

Yu, Misook

To: STIC-Biotech/ChemLib
Subject: 09847102

Please search SEQ ID NO:68 and DNA encoding SEQ ID NO:68.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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OM protein - protein search, using SW model

Run on: May 19, 2003, 16:31:36 ; Search time 36 Seconds

(without alignments)
869.830 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARPDPAPPSLLLLLAQL.....PNCAPCYOPSPFSADERTFA 235

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	585	18	AAW41254
2	824	62.9	694	23	AAU74823
3	823.5	62.9	685	18	AAW41274
4	621	47.4	694	18	AAW41267
5	621	47.4	694	22	ABR71797
6	440.5	33.6	572	18	AAW41273
7	415	31.7	647	21	AAW41217
8	384	29.3	581	22	AAW41308
9	380	29.0	325	19	AAW41767
10	372	28.4	325	19	AAW48695

11	372	28.4	325	19	AAW41254	Human "Frazzled" f
12	372	28.4	325	20	AAV03229	Amino acid sequenc
13	372	28.4	325	21	AAW410281	Xenopus sp embryo
14	370.5	28.3	582	22	AAW41307	Mouse frizzled fam
15	370	28.2	589	22	ABR71245	Drosophila melanog
16	367	28.0	323	19	AAW41768	Mouse hnfz protein
17	367	28.0	323	19	AAW41253	Mouse "Frazzled" f
18	367	28.0	323	19	ABW57252	Xenopus growth-ind
19	366.5	28.0	319	19	AAW48696	Xenopus growth-ind
20	366	27.9	325	20	AAW48694	Bovine growth-indu
21	366	27.9	325	20	AAV03223	Amino acid sequenc
22	360	27.5	318	19	AAW41251	Xenopus "Frazzled"
23	349	26.6	372	22	AAW6347	Partial human FRAZ
24	349	26.6	372	22	AAW6347	Partial amino acid
25	342.5	26.1	346	22	AAW48183	Human FRAZ2LED pol
26	342.5	26.1	347	20	AAV03231	Amino acid sequenc
27	342.5	26.1	368	19	AAW73508	Human ARG-1639 pro
28	342.5	26.1	368	20	AAV03232	Full length sequen
29	342	26.1	346	21	AAW63911	Bos taurus Frazzle
30	339.5	25.9	368	20	AAW6346	Human FRAZ2LED pro
31	338.5	25.8	346	21	AAW6346	Breast cancer prot
32	338.5	25.8	346	22	AAW6853	Human lung tumour
33	338.5	25.8	346	23	ABG61803	Prostate cancer-as
34	338.5	25.8	346	23	AAW6508	Clone #19118 of lu
35	338.5	25.8	346	23	AAO14432	Human frizzled rel
36	308	23.5	540	21	AAV90903	Human frizzled-4 p
37	304.5	23.2	666	18	AAW31268	Mouse frizzled-3 p
38	299.5	22.9	537	18	AAW31270	Mouse frizzled-4 p
39	299.5	22.9	537	23	ABW57288	Mouse frizzled-4 p
40	297	22.7	338	20	AAV30157	Mouse ischaemic co
41	297	22.7	468	22	ABW12060	Amino acid sequenc
42	297	22.7	468	22	AAV30156	Human frizzled-3 h
43	284	21.7	700	22	ABW59309	Amino acid sequenc
44	284	21.7	700	22	ABW59309	Drosophila melanog
45	282	21.5	704	20	AAV02383	Drosophila G-prote

ALIGNMENTS

RESULT 1
AAW31271 standard; Protein; 585 AA.
ID AAW31271;
XX AAW31271;
AC AAW31271;
DE 27-APR-1998 (first entry)
DT XX
DX Human frizzled-5 protein Mfz5-(Mnt-receptor).
DE XX
DX Mnt receptor; human frizzled-5 protein; Mfz5 gene;
KW signal transduction; cancer; cell growth; cell proliferation.
XX
XX Homo sapiens.
OS
XX
XX W09739357-A1.
PN
XX
PD 23-OCT-1997.
XX
PF 11-APR-1997; 97WO-US06049.
PR 12-APR-1996; 96US-0015307.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Andrew D, Bhanot P, Bink M, Hsieh J, Nathans J;
PI Nussle R, Samos CH, Wangy;
XX WPI: 1997-526631/48.
DR N-PSDB; AAT89889.
XX
PT Identification of Mnt receptor binding modulators - useful for

PT treatment of cancer and growth, development or proliferation related disorders

XX Disclosure; Page 37-39; 61pp; English.

CC This protein comprises the human transmembrane receptor, CC
CC frizzled-5 (Hfz5), encoded by the Hfz5 gene (see AAT88889). It is CC
CC an example of a Wnt receptor. Other novel frizzled family members CC
CC have been identified in human, mouse and Caenorhabditis elegans CC
CC (see AAM31268-74) and are considered also to be Wnt receptors. Wnt CC
CC receptors can be used in a novel, claimed method of screening for CC
CC compounds which modulate the binding of a Wnt polypeptide (secreted CC
CC proteins involved in cell-to-cell signaling) to a Wnt receptor. CC
CC Wnt is involved in (mammary) cancer and other processes involving CC
CC growth, development and proliferation (both normal and abnormal). CC
CC Modulators identified by the claimed method are useful for CC
CC treatment of diseases related to these conditions.

XX Sequence 585 AA;

Query Match 100.0%; Score 1310; DB 18; Length 585;

Best Local Similarity 100.0%; Pred. No. 8.6e-102; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARPDSAPPSLLILLIAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPQFNHDTQ 60

OY 61 DEAGLEHGFVPLVEIQCSBPDLPFLCTMYTPICLPDYHKPLPPCSVCEKAKGCSPLM 120

DB 61 DEAGLEHGFVPLVEIQCSBPDLPFLCTMYTPICLPDYHKPLPPCSVCEKAKGCSPLM 120

OY 121 ROYGFAPMRMSCDRLPVGRDAEVLICMDYNSEATTAPRPPAKPTLPGPAGASAG 180

DB 121 ROYGFAPMRMSCDRLPVGRDAEVLICMDYNSEATTAPRPPAKPTLPGPAGASAG 180

OY 121 ROYGFAPMRMSCDRLPVGRDAEVLICMDYNSEATTAPRPPAKPTLPGPAGASAG 180

DB 121 ROYGFAPMRMSCDRLPVGRDAEVLICMDYNSEATTAPRPPAKPTLPGPAGASAG 180

OY 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

DB 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

OY 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

DB 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

OY 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

DB 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

OY 181 ECPAGGPFVCKCRPEFVPIKESHPLYNKVRGQVNCVPCYQPSFADERTFA 235

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PR 21-JUN-2000; 2000US-214027P.

PR 25-AUG-2000; 2000US-228045P.

PR 12-DEC-2000; 2000US-255104P.

XX (INCY-) INCYTE GENOMICS INC.

XX Griffin JA, Kallik DA, Tribouley CM, Yue H, Nguyen DB, Tang YT,

XX Lal P, Policky JL, Aizawa Y, Lu DM, Graul R, Yao MG, Burford N,

XX Hafalia AJA, Baugh MR, Bandman O, Patterson C, Yang J, Xu Y,

XX Gandhi AR, Warren BA, Ding L, Sanjamaal MS, Duggan BM, Lu Y,

XX WPI; 2002-090432/12.

XX N-PBDB; ABK15174.

XX Twelve human receptors (referred to as REPR-1 to REPR-12), useful in

XX the diagnosis, treatment and prevention of gastrointestinal (e.g.

XX gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell

XX proliferative (e.g. cancer) disorders -

XX Claim 50; Page 119-121, 157pp; English.

XX This invention relates to twelve human receptors CDNA sequences

XX referred to as REPR-1 to REPR-12), and the proteins encoded thereby.

XX The proteins of the invention may have antiinflammatory, cyostatic,

XX immunosuppressive, antiviral, anti-HIV, antidiarrhetic, muscular active

XX general, anticonvulsant, nootropic, neuroprotective, antiallergic

XX activities. The sequences of the invention may be used to produce REPR

XX agonists or antagonists, and the protein sequences may be used to raise

XX anti-REPR antibodies. These molecules and the REPR polynucleotides and

XX polypeptides of the invention are useful in the diagnosis, treatment and

XX prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,

XX Crohn's disease, irritable bowel syndrome, ulcerative colitis),

XX endocrine (e.g. hypothyroidism, diabetes mellitus), autoimmune/

XX inflammatory (e.g. acquired immune deficiency syndrome (AIDS),

XX rheumatoid arthritis, allergies, osteoarthritis, diabetes mellitus,

XX multiple sclerosis, systemic lupus erythematosus), cell proliferative

XX (e.g. cancer), developmental (e.g. Duchenne and Becker muscular

XX dystrophy), neurological (e.g. epilepsy, Alzheimer's disease,

XX Huntington's disease) and reproductive (e.g. infertility, endometriosis)

XX disorders. Numerous other examples of each disorder are given in the

XX specification. The present sequence represents the human REPR6 protein

XX Sequence 694 AA;

Query Match 62.9%; Score 824; DB 23; Length 694;

Best Local Similarity 59.9%; Pred. No. 6.6e-61; Indels 48; Gaps 8;

Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

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DB 11 SLLAALALLQSSGGAASAKELACQELTVPILKIGIGNYTMPQFNHDTQDEAGLEVN 70

OY 69 QFWPLVEIQCSBPDLPFLCTMYTPICLPDYHKPLPPCSVCEKAKGCSPLMROYGFAMP 128

DB 71 QFWPLVEIQCSBPDLPFLCTMYTPICLPDYHKPLPPCSVCEKAKGCSPLMROYGFAMP 130

OY 129 FRMSGCDRLPVGRDAEVLICMDYNSEATTAPRPPAKPTLPGPAGASAG 180

DB 131 DMRCDRLPVGRDAEVLICMDYNSEATTAPRPPAKPTLPGPAGASAG 187

OY 175 A-----PASG-----ECPAGGPFV-----CKCRPEFVPIKESH 205

DB 168 ARPRIRGGGGGGGGAAPARAGGGGGGKARPPGGGAAPRPGGCGCAPVSVSSRHP 247

OY 206 LYNKVRGQVNCVPCYQPSFADERTFA 234

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

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OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

OY 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

DB 248 LYNKVRGQVNCVPCYQPSFADERTFA 276

XX AAM31274;
AC 27-APR-1998 (first entry)
XX
XX Mouse frizzled-8 protein Mfz8 (Wnt receptor).
XX
XX DE Mouse frizzled-8 protein; Mfz8 gene;
XX KM Wnt receptor; mouse frizzled-8 protein; Mfz8 gene;
XX KM signal transduction; cancer; cell growth; cell proliferation.
XX OS Mus musculus.
XX PN W09739357-A1.
XX PD 23-OCT-1997.
XX PF 11-APR-1997; 97WO-US06049.
XX PR 12-APR-1996; 96US-0015307.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
PI Nusse R, Samos CH, Wangy;
XX WPI; 1997-526631/48.
XX DR N-PSDB; AAT89892.
XX
XX Identification of Wnt receptor binding modulators - useful for
PT treatment of cancer and growth, development or proliferation related
PT disorders
XX
XX Disclosure; Page 48-50; 61pp; English.
XX
XX This protein comprises the mouse transmembrane receptor,
CC frizzled-8 (Mfz8), encoded by the Mfz8 gene (see AAT89892). It is
CC an example of a Wnt receptor. Other novel frizzled family members
CC have been identified in human, mouse and Caenorhabditis elegans
CC (see AAM31268-74) and are considered also to be Wnt receptors. Wnt
CC receptors can be used in a novel, claimed method of screening for
CC compounds which modulate the binding of a Wnt polypeptide (secreted
CC proteins involved in cell-to-cell signaling) to a Wnt receptor.
CC Wnt is involved in (mammary) cancer and other processes involving
CC growth, development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.
XX
XX Sequence 685 AA;
SQ
Query Match 62.9%; Score 823.5; DB 18; Length 685;
Best Local Similarity 60.0%; Pred. No. 7.2e-61;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
QY 11 SLV--LILLALVGRGAASAPVCQBITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVH 68
DB 11 SLIALAVLQSSSGAASAKELACQBITVPLCKSIGNYTMRQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSBDLRFCTMTPTICLDYHAKPLPPCSVCERAAAGCSPLMRQYGFAMP 128
DB 71 QFWPLVEIQCSBDLRFCTMTPTICLDYHAKPLPPCSVCERAAAGCSPLMRQYGFAMP 130
QY 129 ERMSCDRLPVGRDAEVCMQDNRSEATTA---PPRPPAKPTLGG-----PPG 174
DB 131 DRMRCDRLPEQG-NPDTICMDYNRDITLTAAPSPPRLPPPP-PEGQPPSGSGSRPPG 188
QY 175 A-----PASGEC--PAGGPFV---CKRBPFPVILKESHPLYNK 209
DB 189 ARPHRGSSSGSDAAAPPSRGKARPPGGGAAPCEGCGCRAPMTSVSESRHPLYNR 248
QY 210 VRTGQVPCAVPCYQPSFADRTF 234
DB 249 VKTGOIANCALPCNHPFSQDERAF 273

RESULT 4
AAM31267
ID AAM31267 standard; Protein; 694 AA.
XX
XX AAM31267;
AC 27-APR-1998 (first entry)
XX
XX DE Drosophila frizzled-2 protein (Wnt receptor).
XX KM Wnt receptor; Drosophila frizzled-2 protein; Dfz2 gene;
XX KM wingless receptor; Wg receptor; signal transduction; cancer;
XX KM cell growth; cell proliferation.
XX OS Drosophila melanogaster.
XX
XX Key Location/Qualifiers
FH Misc-difference 268
FT /note= "encoded by CAC"
FT Misc-difference 269
FT /note= "encoded by TGC"
FT Misc-difference 348
FT /note= "encoded by TA (apparent 1 nucleotide
FT deletion of codon)"
FT Misc-difference 488
FT /note= "encoded by TTA"
FT Misc-difference 632
FT /note= "encoded by CTG"
FT Misc-difference 633
FT /note= "encoded by GCG"
FT Misc-difference 671
FT /note= "encoded by CG (apparent 1 nucleotide
FT deletion of codon)"
XX
XX W09739357-A1.
XX
XX 23-OCT-1997.
XX
XX 11-APR-1997; 97WO-US06049.
XX
XX 12-APR-1996; 96US-0015307.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
XX PI Nusse R, Samos CH, Wangy;
XX
XX WPI; 1997-526631/48.
XX DR N-PSDB; AAT89885.
XX
XX Identification of Wnt receptor binding modulators - useful for
PT treatment of cancer and growth, development or proliferation related
PT disorders
XX
XX Claim 2; Page 23-25; 61pp; English.
XX
XX This protein comprises the Drosophila frizzled-2 protein encoded by
CC the Dfz2 gene (see AAT89885). It is a receptor for wingless (Wg),
CC acting as a signal transducing molecule, and is an example of a Wnt
CC receptor (WntR). Other novel frizzled family members have been
CC identified in human, mouse and Caenorhabditis elegans (see
CC AAM31268-74) and are considered also to be Wnt receptors. Wnt
CC receptors can be used in a novel, claimed method of screening for
CC compounds which modulate the binding of a Wnt polypeptide (secreted
CC proteins involved in cell-to-cell signaling) to a Wnt receptor.
CC Wnt is involved in (mammary) cancer and other processes involving
CC growth, development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.
XX

Seq	Sequence	694 AA;
Query Match	47.4%;	Score 621; DB 18; Length 694;
Best Local Similarity	43.4%;	Pred. No. 7.3e-44;
Matches 124; Conservative	27;	Mismatches 55; Indels 80; Gaps 7;
QY	22 GRAAASAKAP-----VCEITVPMCRGIGYNLTTHMPNPFNHTODEAGLEVAH 68	
DB	40 GHGLDASPAPDGVPAIPDPDPLNRCEIITIPMCRGIGYNNTSPNPMNHETODEAGLEVAH 99	
QY	69 QPWLVEIQCSPDLRFFLCSTMYTPIPLPDYHKPLPFCRSVCEAKAGSPLMROYFAMP 128	
DB	100 QPWLVEIKCSPDLKFFLCSTMYTPILEBYHKPLPFCRSVCEAKAGSPLMQYFEMP 159	
QY	129 ERMSCDRLPVLGRDDEVLCMDY----- 150	
DB	160 ERMACEHPLFLH-DPDLNLCEQPSYTEAGSGSGSGSGSGSGSGGKRRKQSGSGGS 218	
QY	151 ----NRSEATTPPPPPFAKPTLPGRGAPASGCGEPAGGPFVCKRREP----- 197	
DB	219 GAGSGSGSTSTPCKGRNSK-NCONQKASGKES-----CSCRSPILFLGKEQLIQ 271	
QY	198 ----PIKESHPLYNKV---RTGQVPNCADVPCYQPSFADERTFA 235	
DB	272 QQSQPMHMHPPHMYMNLVQRIAGVPNGICPKCGFFFNDEKDF 317	
RESULT 5		
ABBT1797		
ID	ABBT1797 standard; Protein; 694 AA.	
XX	ABBT1797;	
AC		
XX	26-MAR-2002 (first entry)	
DT		
XX	Drosophila melanogaster polypeptide SEQ ID NO 42183.	
DE		
XX	Drosophila; developmental biology; cell signalling; insecticide;	
KW	pharmaceutical.	
KM		
XX	Drosophila melanogaster.	
OS	WO200171042-A2.	
XX		
PN	27-SEP-2001.	
PD		
XX	23-MAR-2001; 2001WO-US09231.	
PF		
XX	23-MAR-2000; 2000US-191637P.	
PR	11-JUL-2000; 2000US-0614150.	
XX		
XX	(PEKE) PE CORP NY.	
PA		
XX		
PI	Venter JC, Adams M, Li PWD, Myers EW;	
XX	WPI; 2001-656860/75.	
DR	N-PSDB; ABL15900.	
XX		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more	
PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
PT	interactions -	
XX		
XX	Disclosure; SEQ ID NO 42183; 21pp + Sequence Listing; English.	
PS		
XX		
CC	The invention relates to an isolated nucleic acid detection reagent	
CC	capable of detecting 1000 or more genes from Drosophila. The invention is	
CC	useful in developmental biology and in elucidating cell signalling and	
CC	cell-cell interactions in higher eukaryotes for the development of	
CC	insecticides, therapeutics and pharmaceutical drugs. The invention	
CC	discloses genomic DNA sequences (AB116176-AB130511), expressed DNA	
CC	sequences (AB101840-AB116175) and the encoded proteins	
CC	(AB57737-AB72072).	
CC	The sequence data for this patent did not form part of the printed	

CC specification, but was obtained in electronic format directly from WIPD.
at ftp.wipo.int/pub/published_pct_sequences.

XX
XX

SQ Sequence 694 AA;

Query Match 47.4%; Score 621; DB 22; Length 694;
Best Local Similarity 43.4%; Pred. No. 7,3e-44;
Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps

OY 22 GRAAASAKP-----VQEIITVMCRIGYNLTMPNQFMHDTQDEAGLEVN 68
| | | | | : | | | | | : | | | | |
DB 40 GHGDASPAPGVGVIVPKDPNLRCEBITIIMCRGIGNMTSFPENMNHETQDEAGLEVH 99
OY 69 QFWPLVEIQCSBDLRFELCTMYTPIFLCPDYHKPLPPCKSVCEBAACGSPLMKRYGFAMP 128
| | | | | : | | | | | : | | | | |
DB 100 QFWPLVEIKCSBDLRFELCMTPTICLEDYHKPLPVCRSVCEBARSGCAPIMQYSFEMP 159
OY 129 ERMSCDRLPVIGRDAEVLCMY----- 150
| | | | | : | | | | | : | | | | |
DB 160 ERMCEHLPLHG-DPDNLCHMQPSTTEAGSGSSGGSGSGSGSGSKRGKOGSGSGGS 218
OY 151 ---NRSEATTAPRPFPFAKPTLPGPAPAPASGGECPAGPFVCKCREPFV----- 197
DB 219 GAGSGSGSTSRKPCGRNSK-NCQNPQEKASGKECS-----GCRSPPLIFLGEQLLQ 271
OY 198 ----PILKESHPLYNKV---RTGOVPNCANPCIOPSADERTPA 235
| | | | | : | | | | | : | | | | |
DB 272 QQSQPMWMMHPHHWMYMLTVQRIGAVGPCGIPCKGFFFSNDKDFPA 317

RESULT 6
AAW31273
ID AAW31273 standard; Protein; 572 AA.
XX
XX AAW31273;
XX AC
XX DT 27-APR-1998 (first entry)
XX DE Mouse frizzled-7 protein Mfz7 (Wnt receptor).
XX KW Wnt receptor; mouse frizzled-7 protein; Mfz7 gene;
XX KM signal transduction; cancer; cell growth; cell proliferation.
XX OS Mus musculus.
XX PN MO97339357-A1.
XX PD 23-OCT-1997.
XX PF 11-APR-1997; 97MO-US06049.
XX PR 12-APR-1996; 96US-0015307.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
XX PI Nussle R, Samos CH, Wangy;
XX WP1: 1997-5526631/48.
XX DR N-PDSB; AAT89891.
XX PT Identification of Wnt receptor binding modulators - useful for
XX treatment of cancer and growth, development or proliferation related
XX disorders
XX
XX PS Disclosure; Page 44-46; 61pp; English.
XX
XX This protein comprises the mouse transmembrane receptor,
XX frizzled-7 (Mfz7), encoded by the Mfz7 gene (see AAT89891) . It is
XX an example of a Wnt receptor. Other novel frizzled family members
XX have been identified in human, mouse and Caenorhabditis elegans
XX (see AAW31266-74) and are considered also to be Wnt receptors. Wnt

CC receptors can be used in a novel, claimed method of screening for
CC compounds which modulate the binding of a Wnt polypeptide (secreted
CC proteins involved in cell-to-cell signalling) to a Wnt receptor.
CC Wnt is involved in (mammary) cancer and other processes involving
CC growth, development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.
CY

SQ Sequence 572 AA;

Query Match	33.6%	Score 440.5;	DB 18;	Length 572;
Best Local Similarity	38.8%;	Pred. No. 8.4e-29;		
Matches 100; Conservative	36;	Mismatches 75;	Indels 47;	Gaps 12;

QY 8 APPSILLILLIQLVGRAAAASKAP-----VCOEIVLMCRGIGYLLTHMPN 53
 Db 11 SPLGLCAVLTA-LTGALEPTDRAQRYHGEKGISVBDHGFQGISIPCTDIANYQTILPN 69
 QY 54 QFNHDTODEALEYHNFQPIVEIICSPRLRFLCTMTPTICLRPDYHKLPRCSVSERAK 113
 Db 70 LLGHTNGDDEAGLEHNFQPIVLKVCOSPEPLRFLCTSMARVSTV-LDQKIPCRSLCEAR 128

QY 114 AGCSELMKRGVGFAPBEMSCDRLEVLORDAEVICMDVNBSEAR----TAPRPAPAPLP 170
 Db 129 QGCEALNNKKGFGFQPERLRRCENFVHG--AGEICVCGNTSDGSGGAGSPTAPRAPLP 186
 QY 171 GPFPAPASGGECPAGCG-----PVCRCREPFPIILKESHPLYNKVRGTGVPCAVPCQ 224
 Db 187 DEPTAMS----PEDGGRSLSPFSCE-RQLNKP-----PIQYRFLGE-RDCGAPC-E 233
 QY 225 PS-----PSADRTFA 235
 Db 234 PGRANGLMYFGEERRRPA 251

RESULT 7
AAB12117
ID AAB12117 standard; Protein; 647 AA

AAC12117;

DT 02-FEB-2001 (first entry)

Hydrophobic domain protein from clone HP02539 isolated from Saos-2 cells

KM Human secreted protein; membrane protein; hydrophobic domain;
KM proliferation control; differentiation induction; material transport;
KM biophysics; signal receptor; ion channel; transporter; immunostimulant
KM immunosuppressant; haematopoiesis regulator; chemoelectric; chemokinetic;
KM haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
KM autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

Homo sapiens.

PN WO200029448-A2.

PD 25-MAY-2000.

PF 17-NOV-1999; 99WO-JP06412.
VY

PR	17-NOV-1998;	98UP-0326255.
PR	22-DEC-1998;	98UP-0364315.
PR	16-MAR-1999;	99UP-0069811.
PR	27-APR-1999;	99UP-0119229.
PR	19-MAY-1999;	99UP-0138169.

PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
PA

PI Kato S, Kimura T;
.....

DR WPI; 2000-387753/33.
DR N-PSDB; AAA60179, AAA60189.

XX Proteins comprising hydrophobic regions, such as secretory and membrane
 XT proteins, useful in research and diagnostics and having various
 PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
 PT hemostatic, thrombolytic -
 XS Claim 1; Page 178-181; 410pp; English.

Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophysaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer.

SQ Sequence 647 AA;

Query Match	31.7%;	Score 415;	DB 21;	Length 647;
Best Local Similarity	36.0%;	Pred. No. 1.3e-26;		
Matches 104;	Conservative 30;	Mismatches 87;	Indels 68;	Gaps 11;

```

3 RP--DPSAPSLLLLL-----AQLVG-RAAAASKAP----- 31

```

Db 43 RPPVDPRRLARQLLLTWLLEAPLLGVRAQAAGCGPGCGQPPPPPPQQQSGQQY 102

32 -----VCQEI TVPMCRGIGY NLTHMPNQFNHDTQDEAGLEVHQFWPLVEIQCS 75

Db 103 NGERGISVPDHGXCQPI S I P L C T D I A Y N Q T I M P N L L G H T N Q E D A G L E V H Q F Y P L V K V Q C S 162

80 PDLRFFLCTMYTICLPDYHKLPPCRSVCKERAKAGCSPLMRQYGFAPPERMSCDRLPVL 133

Db 163 AELKFFLCSMYAPVCTV-LEQALPPCRSLCERARQGCCEALMNKFGFQWPDTLKCEKFPVH 221

QY 140 GRDAEVL CMDYNRSEATTAPRPPFPAKPTLP GPPGAPASGGECPPAG-----GPFVCKCR 193

Db 222 G--AGELCVGQNTSDKGTPTPSLLPFWTSNPQHGCGHRCGFPGGAGASERGKFSR-R 278

194 BPFPVPIKESHPLYNKVRTGVPNCVPCYOPS-----FSADERTFA 2335

Db 279 ALKVPSYLNHYFLGEK-----DCGAPC-EPTKVYGLMYFGPEELRFS 319

DEPT 3

AAB73308
ID AAB73308 standard; Protein; 581 AA

AC AAB73308 ;

DT 22-MAY-2001 (first entry)

Human frizzled family protein 584

KM Human; frizzled family gene 584; embryo; foetus; cancer;
KM drug discovery; cytostatic.

OS Homo sapiens

PN WO200112808-A1
 YY

PD 22-FEB-2001.
yy

PF 18-AUG-2000; 2000WO-JP05552

PR 18-AUG-1999; 99JP-0232018

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC

XX Senoo C, Numata M;
 XX WPI: 2001-211220/21.
 DR N-PSDB: AAF75974.
 XX Novel frizzled family genes 584 strongly expressed in embryo and fetus
 PT as well as in cancer cells; useful in drug development for diseases
 PT with abnormal expression including tumor
 XX
 PS Claim 1; Fig 6-7; 89pp; Japanese.
 CC The invention relates to a novel frizzled family gene, 584, from mouse
 CC and human (CDNAs given in AAF75973 and AAF75974), and to the mouse and
 CC human 584 proteins (AAF73307, AAF73308). Gene 584 is strongly expressed
 CC in the embryo and foetus, and is also strongly expressed in cancer
 CC cells. The invention also relates to recombinant vectors and host
 CC cells comprising gene 584 nucleic acids, the recombinant expression of
 CC the 584 protein, methods of screening for modulators of 584 activity or
 CC expression, and the compounds thus identified. The human and mouse 584
 CC genes represent a novel gene target for the development of drugs useful
 CC in the treatment of diseases such as cancer. The present sequence
 CC represents human protein 584.
 CC
 XX Sequence 581 AA;
 SQ
 Query Match 29.3%; Score 384; DB 22; Length 581;
 Best Local Similarity 39.6%; Pred. No. 4,8e-24;
 Matches 82; Conservative 27; Mismatches 70; Indels 28; Gaps 7;
 QY 1 MARPPSAAPSLILLILLALQVGRAAAASKAPV-----CGEITVPMCRGIGYNTLTHMPN 53
 DB 1 MORPSPR-----LMLVLIQVMGSCAIISSMDMERPGDGKCPLEIIMCKDIDGYNMTMPN 54
 QY 54 QENHTDDEAGLEVFQFMPLVEIQCSPLRFLCTMYTPICLPDYHKPLPPCRSVCERAK 113
 DB 55 LMGHNNORBAALQHEFAPLVVYGGHLPFLCSLYAMCTEOVSTPIPAKRWCEQAR 114
 QY 114 AGCSPLMROYGFAMPERMSCDRLPVILGRDAEVLCMD--YNRSEATY-----APPR 161
 DB 115 LKCSPIIMQFNFKWPDSDLCRKL-P-NKNDPNYLCKEAPNNGSDEFTRGSGLPPLPRPQR 173
 QY 162 PPPAKPTLPGPPGAPASGGCECPAGGPF 188
 DB 174 PHSAQEH-PLKDGPGRGG-CPNPGKF 198
 RESULT 9
 AAM41767
 ID AAM41767 standard; Protein; 325 AA.
 AC AAM41767;
 XX
 DT 28-SEP-1998 (first entry).
 DE Human hsfz protein.
 XX
 KM Human; nerve cell growth factor; hsfz protein; neuronal cell;
 KM proliferation; differentiation factor.
 OS Homo sapiens.
 PN DE19702835-A1.
 PD 22-JAN-1998.
 PF 27-JAN-1997; 97DE-1002835.
 PR 09-JUL-1996; 96DE-1027631.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX Deutsch U. Drexler JCA, Lottspeich F, Mayr T, Risseu W;
 PI

PI Rohrer H;
 XX
 DR WPI: 1998-088096/09.
 DR N-PSDB: AAV13101.
 XX New nucleic acid encoding protein that increases neuronal cell
 PT proliferation - useful as nerve growth factor and for detection or
 PT inhibition of differentiation factors
 XX
 PS Claim 5; Page 17; 27pp; German.
 CC This sequence represents the human hsfz protein. This protein is found to
 CC increase the proliferation of neuronal cells. Such proteins can be used
 CC as nerve cell growth factors and for the detection and/or inhibition of
 CC differentiation factors, specifically those corresponding to the
 CC Drosophila melanogaster wingless or mouse int-1 type.
 CC
 XX Sequence 325 AA;
 SQ
 Query Match 29.0%; Score 380; DB 19; Length 325;
 Best Local Similarity 36.0%; Pred. No. 5,4e-24;
 Matches 81; Conservative 34; Mismatches 80; Indels 30; Gaps 7;
 QY 10 PSLILLILALQVGRAA-----AASKAPVCGEITVPMCRGIGYNTLTHMPNHDQDEA 63
 DB 6 PGMILLRAGLLAALCLLRVPGARAACEPVRIPLCKSLPMWMTKMPNLIHSTQDNA 65
 QY 64 GLEVHQFMPLVEIQCSPLRFLCTMYTPICLPDY-HKPLPPCRSVCERAKAGCSPLMRQ 122
 DB 66 ILAIHQFEGGLGTHCSPLDFFLCAMTAPICTIDFOHEPIPCSVGERARQCEPIIUK 125
 QY 123 YGFAMPERMSCDRLPVILGRDAEVLCMDYNRSEATYAPPRPPAKPTLPGPPGASGGEC 182
 DB 126 YRHSWPENLACEELPVYDRG---VCI--SPEAIVTADGADPP-----MDSNGNC 170
 QY 183 PAGGPVCKREPPVPIIKESHPL-----YKNVKTGOVPCNCAVPCY 223
 DB 171 RGASSERCKCK---PIRATQKTYFRNNYVIRAKVKEIKTKCH 211
 RESULT 10
 AAM48695
 ID AAM48695 standard; Protein; 325 AA.
 AC AAM48695;
 XX
 DT 04-SEP-1998 (first entry)
 DE Human growth-inducing protein Frzb sequence.
 XX
 KM Frzb; growth-inducing protein; bovine; human; Xenopus; cartilage;
 KM bone; nerve; muscle; tumour; Wnt-expressing tumour; myodegeneration;
 KM subglottic stenosis; chondromalacia patellae; osteoarthritis;
 KM joint surface lesion; neurodegeneration; Alzheimer's disease;
 KM osteodegeneration; angiogenesis; wound healing.
 OS Homo sapiens.
 PN WO9816641-A1.
 PD 23-APR-1998.
 PF 08-OCT-1997; 97WO-US18362.
 PR 20-MAR-1997; 97US-082233.
 PR 11-OCT-1996; 96US-0729452.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Hoang B, Luyten FP, Moos M, Wang S;
 XX WPI: 1998-251288/22.
 DR N-PSDB: AAV18254.
 DR

XX New nucleic acid encoding human, bovine and Xenopus Frzb protein -
PT and related proteins, antibodies, peptide(s), vectors and
PT transformed cells, used to induce growth of cartilage, bone, nerve
PT and muscle, also for inhibiting Wnt-expressing tumours
XX
XX Claim 4, Pages 37-38; 66pp; English.

CC This represents a human growth-inducing protein Frzb. Bovine, human
CC and Xenopus Frzb genes which are shown in AAV1825 to AAV1825 are
CC related to the frizzled gene in Drosophila. The corresponding bovine,
CC human and Xenopus Frzb protein sequences are shown in AAV48694 to
CC AAV48696. A recombinant construct containing a Frzb encoding nucleic acid
CC linked to a heterologous promoter in an expression vector can be used to
CC produce recombinant Frzb proteins. The Frzb proteins may be formulated
CC with fibrin glue, freeze-dried cartilage grafts or collagen (optionally
CC also cartilage progenitor cells, chondroblasts or chondrocytes). They
CC are coated on to, or mixed with, a (non-)resorbable matrix, or mixed with
CC a biodegradable polymer. They modulate activity of the growth factors
CC Wnt-1 to 8. The Frzb proteins induce skeletal morphogenesis, embryonic
CC pattern formation and tissue specificity and are used to induce growth
CC of cartilage, bone, nerve and muscle, particularly in cases of
CC subglottic stenosis, chondromalacia patellae, osteoarthritis, joint
CC surface lesions, neurodegeneration (e.g. Alzheimer's disease),
CC myodegeneration or osteodegeneration. They also modulate Wnt-mediated
CC signalling in cells, and are used to inhibit growth of Wnt-expressing
CC tumours (particularly mammary or intestinal). The Frzb genes may also be
CC used to identify specific modulators or as a growth factor for cells of
CC the chondrocyte lineage in vitro, to stimulate wound healing, to promote
CC angiogenesis, to prevent transplant rejection and as adjunct to
CC chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
CC detecting genetic abnormalities associated with Frzb genes.

XX Sequence 325 AA;

Query Match 28.4%; Score 372; DB 19; Length 325;
Best Local Similarity 35.6%; Pred. No. 2.6e-23;
Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

10 PSLILLILAOLVGRRA-----AASKAPVCOEITVPMCRGIVNLTMPNPNHDTODEA 63
Db 6 PGGMLLRAGLALALACLRLVPGARAACEPVRIPLCKSLPMWMTKPNHLHSTQANA 65
Qy 64 GLEVHOFPVLEIQCSPDLRFELCTMTYPICLPDY-HKPLPPCRSVCEERAKAGCSPLMRQ 122
Db 66 ILAIEQFEGGLGTHCSPLDLFLFCAMVAPICTIDFQHEPIPCSVCEERAKAGCEPIIILK 125
Qy 123 YGFAMPERMSCDRLPVLRDAEVLQMDYNRSEATTAPRPPAKPTLPGPGAPASGSEC 182
Db 126 YRHSWPEMLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSNGNC 170
Qy 183 PAGGFVCKCEPFVPIIKESHPL-----YNKVRGQVPCNCAVPCY 223
Db 171 RGASSERCKC---PIRATOKTYFRNNYVIRAKVKEIKTKCH 211

RESULT 11
AAW41254
ID AAW41254 standard; Protein; 325 AA.

XX AAW41254;
XX
XX 09-JUL-1998 (first entry)
XX
XX Human "frazzled" frzb-1.
XX
XX Growth factor; frazzled; frzb-1; Wnts antagonist; human;
XX tumour suppressor; cancer.
XX
XX Homo sapiens.
XX
XX MO9748275-A1.
XX
XX

PD 24-DEC-1997.
XX
XX 19-JUN-1997; 97WO-US10942.
XX
XX 18-JUN-1997; 97US-0878474.
PR 20-JUN-1996; 96US-0020150.
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
XX Boumester T, De Robertis EM;
PI
XX
XX WPI, 1998-062760/06.
DR N-PSDB; AAV14017.
DR
XX
XX

CC New isolated growth factors - with neurotrophic, growth or
PT differentiation factor activity, tumour growth suppressor activity
PT or mesoderm differentiation activity
XX
XX Claim 6; Fig 9; 48pp; English.
PS
XX
XX The present sequence is the human growth factor protein
CC "frazzled" frzb-1. frzb-1 is an antagonist of Wnts in vivo, and
CC thus is believed to find utility as a tumour suppressor gene,
CC since overexpressed Wnt proteins cause cancer. Frzb-1 may also be a
CC useful vehicle for solubilisation and therapeutic delivery of
CC complexed Wnt proteins.

XX Sequence 325 AA;

Query Match 28.4%; Score 372; DB 19; Length 325;
Best Local Similarity 35.6%; Pred. No. 2.6e-23;
Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

10 PSLILLILAOLVGRRA-----AASKAPVCOEITVPMCRGIVNLTMPNPNHDTODEA 63
Db 6 PGGMLLRAGLALALACLRLVPGARAACEPVRIPLCKSLPMWMTKPNHLHSTQANA 65
Qy 64 GLEVHOFPVLEIQCSPDLRFELCTMTYPICLPDY-HKPLPPCRSVCEERAKAGCSPLMRQ 122
Db 66 ILAIEQFEGGLGTHCSPLDLFLFCAMVAPICTIDFQHEPIPCSVCEERAKAGCEPIIILK 125
Qy 123 YGFAMPERMSCDRLPVLRDAEVLQMDYNRSEATTAPRPPAKPTLPGPGAPASGSEC 182
Db 126 YRHSWPEMLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSNGNC 170
Qy 183 PAGGFVCKCEPFVPIIKESHPL-----YNKVRGQVPCNCAVPCY 223
Db 171 RGASSERCKC---PIRATOKTYFRNNYVIRAKVKEIKTKCH 211

RESULT 12
AAV03229
ID AAV03229 standard; Protein; 325 AA.

XX AAV03229;
XX
XX 03-AUG-1999 (first entry)
XX
XX Amino acid sequence of Xenopus clone WA129_21.
XX
XX Xenopus; clone WA129_21; embryo cDNA library; vaccine;
XX nutrition; cytokine; cell proliferation; cell differentiation;
XX immune stimulating; suppression; haematopoiesis; activin; inhibin;
XX chemotactic; chemokine; haemostatic; thrombolytic; cadherin;
XX anti-inflammatory; tumour invasion suppressor; tumour inhibition.
XX
XX Xenopus sp.
XX
XX MO9909061-A1.
XX
XX 25-FEB-1999.
XX
XX 21-AUG-1998; 98WO-US17469.
XX
XX

XX 20-AUG-1998; 98US-0137226.
 PR 21-AUG-1997; 97US-0916041.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Evans C, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Treacy M;
 XX WPI: 1999-190151/16.
 DR N-PSDB; AAX28653.
 XX
 PT New polynucleotides encoding secreted proteins - derived from, e.g.
 PT human fetal kidney, potentially useful as vaccines
 XX
 PS Claim 12; Pages 69-70; 75pp; English.
 CC This is the amino acid sequence of the clone WA129_2i isolated
 CC from Xenopus embryo cDNA library, which has a potential use
 CC as a vaccine. The nucleotides and proteins are predicted to have
 CC biological activities which would make them suitable for treating,
 CC preventing or ameliorating medical conditions in humans and animals,
 CC although no supporting data is given. Suggested activities include
 CC nutritional activity, cytokine and cell proliferation/differentiation
 CC activity, immune stimulating (e.g. as vaccines) or suppressing
 CC activity, haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity,
 CC haemostatic and thrombolytic activity, receptor/ligand activity,
 CC anti-inflammatory activity, cadherin/tumour invasion suppressor
 CC activity, and tumour inhibition activity. The nucleotides are also
 CC stated to be useful for gene therapy.
 CC
 SQ Sequence 325 AA;

Query Match 28.4%; Score 372; DB 20; Length 325;
 Best Local Similarity 35.6%; Pred. No. 2.6e-23;
 Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

OY 10 PSLILLALLAQLVGRRA-----AASKAPVCOEITVPMCGIGVNLTHMPNOFNHDTODEA 63
 Db 6 POGMILLRAGLLAALACLRVPGARAACEPVRIPLCKSLPMNTKMPNHLHSTQANA 65
 OY 64 GLEVHQFWPLVEIQSPDLRFELCTMTYPTICLPDY-HKPLPCCSVCEERAKAGCSPLMRQ 122
 Db 66 ILAIQFEGILGTHCSPLDLFFLCAMVAPICTIDFQHEBPIKCKSVCEERARQGEPIILIK 125
 OY 123 YGFAPPEMSCDRPLVLRGDAVLICMDYNRSEATTAAPRPFPAPKPLTLPGPAPASGCEC 182
 Db 126 YRHSGWPEMLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSSNGNC 170
 OY 183 PAGGFVCKCREPFVPIIKESHPL-----YNKVRTGOVPCAVPCY 223
 Db 171 RGASSERCKCK-----PIRATOKTYFRNNYNYVIRAKVEIKTKCH 211

RESULT 13
 AAB10281
 ID AAB10281 standard; Protein: 325 AA.
 XX
 AC AAB10281;
 XX
 DT 16-NOV-2000 (first entry)
 XX
 DE Xenopus sp embryo protein fragment WA129_1i.
 XX

KM Secreted protein; cytosstatic; immunostimulatory; antimicrobial;
 KM antiviral; immunosuppressive; antiinflammatory; vulnery; cytokine;
 KM cell proliferation; differentiation; regulator; treatment; tumor;
 KM autoimmune disease; inflammatory disorder; wound; microbial infection;
 KM viral disease; graft versus host reaction suppression.
 XX
 OS Xenopus sp..
 XX

PN WO200037630-A1.
 XX 29-JUN-2000.
 PD
 XX
 XX 22-DEC-1999; 99WO-US31005.
 PF
 XX
 PR 23-DEC-1998; 98US-0220876.
 XX
 XX (GEMV) GENETICS INST INC.
 PA
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 XX WPI: 2000-442661/38.
 DR N-PSDB; AAA40573.
 XX
 PT Secreted human proteins AS296-1i and AS34-1i, useful for treating
 PT tumors, autoimmune diseases, inflammatory disorders, wounds, microbial
 PT infections and viral diseases -
 XX
 PS Disclosure; Page 280-281; 293pp; English.
 CC This invention describes novel secreted human proteins (I) which have
 CC cytosstatic, immunostimulatory, antimicrobial, antiviral,
 CC immunosuppressive, antiinflammatory and vulnery activity and which act
 CC as cytokine, cell proliferation or differentiation regulators. (I)
 CC is useful for treating tumors, autoimmune diseases, inflammatory
 CC disorders, wounds, microbial infections and viral diseases. (I) is also
 CC useful for suppressing graft versus host reaction. AAB10226-B10288
 CC represent the secreted proteins encoded by AAA40490-A40580 which are
 CC described in the method of the invention.
 CC
 SQ Sequence 325 AA;

Query Match 28.4%; Score 372; DB 21; Length 325;
 Best Local Similarity 35.6%; Pred. No. 2.6e-23;
 Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

OY 10 PSLILLALLAQLVGRRA-----AASKAPVCOEITVPMCGIGVNLTHMPNOFNHDTODEA 63
 Db 6 POGMILLRAGLLAALACLRVPGARAACEPVRIPLCKSLPMNTKMPNHLHSTQANA 65
 OY 64 GLEVHQFWPLVEIQSPDLRFELCTMTYPTICLPDY-HKPLPCCSVCEERAKAGCSPLMRQ 122
 Db 66 ILAIQFEGILGTHCSPLDLFFLCAMVAPICTIDFQHEBPIKCKSVCEERARQGEPIILIK 125
 OY 123 YGFAPPEMSCDRPLVLRGDAVLICMDYNRSEATTAAPRPFPAPKPLTLPGPAPASGCEC 182
 Db 126 YRHSGWPEMLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSSNGNC 170
 OY 183 PAGGFVCKCREPFVPIIKESHPL-----YNKVRTGOVPCAVPCY 223
 Db 171 RGASSERCKCK-----PIRATOKTYFRNNYNYVIRAKVEIKTKCH 211

RESULT 14
 AAB73307
 ID AAB73307 standard; Protein: 582 AA.
 XX
 AC AAB73307;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Mouse frizzled family protein 584.
 XX

KM Mouse; murine; frizzled family gene 584; embryo; foetus; cancer;
 KM drug discovery; cytosstatic.
 KM
 OS Mus musculus.
 XX
 EN WO200112808-A1.
 XX
 PD 22-FEB-2001.

XX 18-AUG-2000; 2000WO-JP05552.
XX PF
XX 18-AUG-1999; 99JP-0232018.
XX PR
XX (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PA
XX Senoo C, Numata M;
XX PI
XX WPI; 2001-211220/21.
XX DR N-PSDB; AAF75973.
XX PT Novel frizzled family genes 584 strongly expressed in embryo and fetus
XX PT as well as in cancer cells; useful in drug development for diseases
XX PT with abnormal expression including tumor -
XX PS
XX Claim 1; Fig 1; 89pp; Japanese.
XX CC The invention relates to a novel frizzled family gene, 584, from mouse
XX CC and human (cDNAs given in AAF75973 and AAF75974), and to the mouse and
XX CC human 584 proteins (AAF7307, AAF7308). Gene 584 is strongly expressed
XX CC in the embryo and fetus, and is also strongly expressed in cancer
XX CC cells. The invention also relates to recombinant vectors and host
XX CC cells comprising gene 584 nucleic acids; the recombinant expression of
XX CC the 584 protein, methods of screening for modulators of 584 activity or
XX CC expression, and the compounds thus identified. The human and mouse 584
XX CC genes represent a novel gene target for the development of drugs useful
XX CC in the treatment of diseases such as cancer. The present sequence
XX CC represents mouse protein 584.
XX SQ
SQ Sequence 582 AA;
Query Match 28.3%; Score 370.5; DB 22; Length 582;
Best Local Similarity 34.9%; Pred. No. 6.5e-23;
Matches 87; Conservative 34; Mismatches 93; Indels 35; Gaps 10;
QY 1 MARPPSAPPELLLLLLQLVGRRAAASKAVY-----COEITVPMCRGIGYNTLHMPN 53
DB 1 MOHPBP-----LMLVLQVMIGSCTAISSMDLERPGDCQVEIIPCKDIGNYTRMPN 55
QY 54 QFNHDTQDAGLEVNQFPLVEIQSPDLRFCTMTYPICLPDKHKLPPRSCBNAK 113
DB 56 LMGHNQDEALIQLEHFAVLVEYGHSLRFPLCSLVAPMCTEQYSTPIACRVNCEQAR 115
QY 114 AGCSPLMQYGFAMPBRMSCDRLPVLGRDAEVLAMD--YNRSEATTAPRPPAKPTLP 171
DB 116 LKCSIMQFRRWPSDLSCKLP-NKNDPNTLCMEAPNNSDESRSGMFP--PLP-- 170
QY 172 PPGAPASGGECPA--GGPFVCKCREPFVPIKESHPLYNKVTGVPNCA--VPCYOPS 226
DB 171 RPRPHSAQEHPLKDGCGRAGCDNP-----GKFNHVKSE--SCAPLCGTGVVY 219
QY 227 FSADERTFA 235
DB 220 WSRDDKRA 228
RESULT 15
ABB71245
ID ABB71245 standard; Protein, 589 AA.
XX ABB71245;
XX AC
XX 26-MAR-2002 (first entry)
XX DT
XX Drosophila melanogaster polypeptide SEQ ID NO 40527.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX XX
XX PN W0200171042-A2.

XX 27-SEP-2001.
XX PD
XX 23-MAR-2001; 2001WO-US09231.
XX XX
XX PF
XX 23-MAR-2000; 2000US-191637P.
XX PR
XX 11-JUL-2000; 2000US-0614150.
XX PR
XX (PEKE) PE CORP NY.
XX PA
XX Venter JC, Adams M, Li PWD, Myers EW;
XX PI
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL15348.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS
XX Disclosure; SEQ ID NO 40527; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
XX CC sequences (ABL101840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX CC
XX SQ
SQ Sequence 589 AA;
Query Match 28.2%; Score 370; DB 22; Length 589;
Best Local Similarity 40.9%; Pred. No. 7.2e-23;
Matches 85; Conservative 29; Mismatches 72; Indels 22; Gaps 9;
QY 33 COEITVPMCRGIGYNTLHMPNQFNHDTQDAGLEVNQFPLVEIQSPDLRFPLCTMYTP 92
DB 53 CEPITISTCKNIPYNMTIMPNTLWIKTQDEAGLEVNQFAPLVKIGSSDDLPLFCSLYTP 112
QY 93 ICLPDYHKLPLPCRSVCERAKAGCSPLMROYGFAMPBRMSCDRLPVLGRDAEVLAMDYN 151
DB 113 VC-TILERPPIPCSLCESARV-CEKLMKTYNFMFNPENLBCSKRPVNG--GEDICVAEMT 168
QY 152 -RSEATTAPRPPAKPTLPGPAPASGGECPAGG--PFVCKCREPFVPI-LKESHPLYN 208
DB 169 TSSASTATPTRSVAKVT---TRKHQTGVESPHRNIGFVC-----PVQLKXTPPLGMGY 217
QY 209 KVRTG---QVNCAPVPCQPSFADERT 233
DB 218 ELKVGKQDLHDGAPCHAMFFPERERT 245

Search completed: May 19, 2003, 16:34:12
Job time : 39 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:33:37 ; Search time 15 Seconds
(without alignments)
460,959 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPPSPAPSLLLLLLAQ.....PNCAPCYPSFSADERTFA 235

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	585	4	US-08-937-067-9
2	823.5	62.9	685	4	US-08-937-067-14
3	477	36.4	565	4	US-08-937-067-8
4	440.5	33.6	572	4	US-08-937-067-13
5	372	28.4	325	4	US-08-878-474-9
6	367	28.0	323	4	US-08-878-474-7
7	360	27.5	318	4	US-08-878-474-3
8	304.5	23.2	666	4	US-08-937-067-10
9	289.5	22.9	537	4	US-08-937-067-11
10	282	21.5	706	2	US-08-987-289-2
11	278.5	21.3	295	4	US-08-937-067-2
12	271	20.7	709	4	US-08-937-067-12
13	270	20.6	212	4	US-08-937-067-4
14	270	20.6	317	4	US-08-937-067-6
15	244.5	18.7	295	4	US-08-893-654B-6
16	234	17.9	314	4	US-08-937-067-7
17	231.5	17.7	281	4	US-08-893-654B-2
18	229	17.5	280	4	US-08-893-654B-4
19	180.5	13.8	641	4	US-09-233-989-10
20	139.5	10.6	787	2	US-08-720-484A-4
21	139.5	10.6	787	4	US-08-953-823A-4
22	139.5	10.6	787	4	US-09-358-239-4
23	130	9.9	793	2	US-08-720-484A-2
24	130	9.9	793	4	US-08-953-823A-2
25	130	9.9	793	4	US-09-293-505-16
26	130	9.9	793	4	US-09-293-505-17
27	130	9.9	793	4	US-09-358-239-2

28	130	9.9	803	4	US-09-293-505-15	Sequence 15, Appl
29	97.5	7.4	1461	4	US-09-585-887-9	Sequence 9, Appl
30	97.5	7.4	1461	4	US-09-289-578-9	Sequence 9, Appl
31	95.5	7.3	265	4	US-08-918-288-39	Sequence 39, Appl
32	95.5	7.3	265	4	US-09-282-357-39	Sequence 39, Appl
33	95	7.3	265	4	US-08-918-288-3	Sequence 3, Appl
34	95	7.3	265	4	US-09-282-357-3	Sequence 3, Appl
35	94.5	7.2	869	2	US-08-644-271-29	Sequence 16, Appl
36	94.5	7.2	869	4	US-08-374-834-16	Sequence 3, Appl
37	94.5	7.2	869	4	US-09-077-955-33	Sequence 29, Appl
38	93.5	7.1	585	4	US-09-930-181-4	Sequence 33, Appl
39	93.5	7.1	603	4	US-09-930-181-17	Sequence 4, Appl
40	93.5	7.1	668	4	US-09-930-181-2	Sequence 1, Appl
41	92	7.0	160	1	US-08-479-233-11	Sequence 2, Appl
42	92	7.0	160	5	PCT-US93-00643-11	Sequence 11, Appl
43	92	7.0	902	1	US-08-396-479B-6	Sequence 6, Appl
44	92	7.0	902	1	US-08-818-823-6	Sequence 6, Appl
45	90	6.9	868	5	PCT-US95-08493-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-937-067-9
Sequence 9, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-9
Query Match 100.0%; Score 1310; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.9e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPPSPAPSLLLLLLAQVGRRAAASKAPVCCQETVPMCRGIGYVLTMPNPFNHDQ 60
DB 1 MARPPSPAPSLLLLLLAQVGRRAAASKAPVCCQETVPMCRGIGYVLTMPNPFNHDQ 60

QY 61 DEAGLEVHOFMWPLVEIQCSFDLRFLLCTMYTPICLPDYHKKPLPPCRSVGERAKAGCSPLM 120
 DB 61 DEAGLEVHOFMWPLVEIQCSFDLRFLLCTMYTPICLPDYHKKPLPPCRSVGERAKAGCSPLM 120
 QY 121 ROYGFAMPERMSCDRLPVIGRDAEVLICMDYNSEATTAAPRPPPAKPTLPGGPGAPASGG 180
 DB 121 ROYGFAMPERMSCDRLPVIGRDAEVLICMDYNSEATTAAPRPPPAKPTLPGGPGAPASGG 180
 QY 181 ECPAGGPFVCKREPFVPLIKESHPLVYKVRGTGVPNCVPCQSPFSADERTFA 235
 DB 181 ECPAGGPFVCKREPFVPLIKESHPLVYKVRGTGVPNCVPCQSPFSADERTFA 235

RESULT 2

US-08-937-067-14
 ; Sequence 14, Application US/08937067
 ; Patent No. 6433155
 ; GENERAL INFORMATION:
 ; APPLICANT: Umansky, Samuil
 ; APPLICANT: Melkonyan, Hovsep
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,067
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lehnhardt, Susan K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20018.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 813-5600
 ; TELEFAX: (650) 494-0792
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 685 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-937-067-14

Query Match 62.9%; Score 823.5; DB 4; Length 685;

Best Local Similarity 60.0%; Pred. No. 2.4e-69; Indels 43; Gaps 8;

Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

QY 11 SLI--LLLLAQLVGRRAAASAKAPVCOEITVPMCRGIGYNTLTPNQFNHDTODEAGLEVH 68
 DB 11 SLI--LLLLAQLVGRRAAASAKAPVCOEITVPMCRGIGYNTLTPNQFNHDTODEAGLEVH 68
 QY 69 QFWPLVEIQCSFDLRFLLCTMYTPICLPDYHKKPLPPCRSVGERAKAGCSPLMROYGFAMP 128
 DB 71 QFWPLVEIQCSFDLRFLLCTMYTPICLPDYHKKPLPPCRSVGERAKAGCSPLMROYGFAMP 130
 QY 129 ERMSCDRLPVIGRDAEVLICMDYNSEATTA--PPRPPPAKPTLP-----PPG 174
 DB 131 ERMSCDRLPVIGRDAEVLICMDYNSEATTA--PPRPPPAKPTLP-----PPG 174

QY 175 A-----PASGSEC--PAGGPFV-----CKREPFVPLIKESHPLVYK 209
 DB 189 ARPPHGGSSSGSGDAAPPSRGCKARPPCGGAAPCEGQCRAPMVSVSEHRLPLYNR 248
 QY 210 VRTGVPCVAVPCVQSPFSADERTF 234
 DB 249 VKTQIANCALPCNHPFSODERAF 273

RESULT 3

US-08-937-067-8
 ; Sequence 8, Application US/08937067
 ; Patent No. 6433155
 ; GENERAL INFORMATION:
 ; APPLICANT: Umansky, Samuil
 ; APPLICANT: Melkonyan, Hovsep
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,067
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lehnhardt, Susan K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20018.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 813-5600
 ; TELEFAX: (650) 494-0792
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 565 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-937-067-8

Query Match 36.4%; Score 477; DB 4; Length 565;

Best Local Similarity 41.9%; Pred. No. 6.7e-37; Indels 40; Gaps 11;

Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RPDSSAPPSLLLLLAQLVGRRAAASAKAPV-----COEITVPMCRGIGYNTLTPNQF 55
 DB 2 RPDSSAPPSLLLLLAQLVGRRAAASAKAPV-----COEITVPMCRGIGYNTLTPNQF 55
 QY 56 NHDQDEAGLEVHOFMWPLVEIQCSFDLRFLLCTMYTPICLPDYHKKPLPPCRSVGERAKAG 115
 DB 62 GHTNQDEAGLEVHOFMWPLVEIQCSFDLRFLLCTMYTPICLPDYHKKPLPPCRSVGERAKAG 120
 QY 116 CSPLMROYGFAMPERMSCDRLPVIGRDAEVLICMDYNSE-----ATTAPRPPPA-KPT 168
 DB 121 CEALMNKKGFWPRLTCEHPRRHG--AEQICVQGNHSEEDGAPALLTTAP--PGIQPG 175
 QY 169 LRGPPGAPASGGECPAGS-----PFVCKREPFVPLIKESHPLVYKVRGTGVPNCVAVPCYQ 224
 DB 176 AGGTPGGGGGAGAPRYATLLEHPHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226
 QY 225 PS-----PSADERTFA 235

Db 227 PARPDGSMFSCQETRFA 244

RESULT 4

US-08-937-067-13

Sequence 13, Application US/08937067

Patent No. 643315

GENERAL INFORMATION:

APPLICANT: Umansky, Samuel

APPLICANT: Melkonian, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 572 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-937-067-13

Query Match 33.6%; Score 440.5; DB 4; Length 572;
Best Local Similarity 38.8%; Pred. No. 1.8e-33;
Matches 100; Conservative 36; Mismatches 75; Indels 47; Gaps 12;

QY 8 APPSLLLLLLLAOLVGRRAAASKAP-----VCOEITVPMCRGIGYNLTMPN 53
Db 11 SPLGLCALVLA-LGALPTDTRADQYHKEGISTVDHFCOPISTPLDTDAHNOTIIPN 69

QY 54 QFNHDQDEAGLEVHQPVLVEIQSPDLRFFELCTMTYPTICLPDYHKEPLPCRSVCERAK 113
Db 70 LLGHTNODAGLEVHQPVLVVKVQSPDLRFFELCSMYAPVCTV-LDQAIPCRSICERAR 128

QY 114 AGCSPLMRQVGFAMPERMSCRLPLTGRDAVLCDMDYRSEAT--TAPPPFPKAPLPLP 170
Db 129 QGCEALMKKFFQWPERLRCENFPVHG--AGEICVQNTSGSGAGSPYAPYAPLPLP 186

QY 171 GPFGAPASGSGCEPAGG-----PFVCKCREPFPVPLIKESHPLYNKRTGOVNCAPCYO 224
Db 187 DPPTAMS-----PSDGRRLSFPSPCP-RQLKVP-----PYLGTRFLGE-RDCGAPC-E 233

QY 225 PS-----PSADERTFA 235
Db 234 PGRANGLMYFKEERRFA 251

RESULT 5

US-08-878-474-9
Sequence 9, Application US/08878474
Patent No. 6133232

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

APPLICANT: Boumeester, Lewis

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

TITLE OF INVENTION: Factors

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hase

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: U.S.A.

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878,474

FILING DATE: 18-JUN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/020,150

FILING DATE: 20-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Siebert, J. Suzanne

REGISTRATION NUMBER: 28,758

REFERENCE/DOCKET NUMBER: 3100.002US1

TELEPHONE: 415/248-5500

TELEFAX: 415/362-5418

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-878-474-9

Query Match 28.4%; Score 372; DB 4; Length 325;
Best Local Similarity 35.6%; Pred. No. 2.5e-27;
Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

QY 10 PSLILLLLLAOLVGRRAA-----AASKAPVCOEITVPMCRGIGYNLTMPN 63
Db 6 PGMILLRAGLLAALAACTLRVPGARAACEPVRIPLCKSLPMNMTKIPNHLHSTQANA 65

QY 64 GLEHOFMPVLVEIQSPDLRFFELCTMTYPTICLPDY-HKPLPFCRSVGERAAGSPMLRQ 122
Db 66 ILAIEQEGGLGTHCSPLDLFFELCMAYAPICTIDFQHEPIPCRSVGERAAGGEPILIK 125

QY 123 YGFAMPERMSCDLPLVGRDAVLCDMDYRSEATTAPPPFPKAPLPLPGRGAPASGCEC 182
Db 126 YRHSMPENLACEELPYVDRG---VCI---SPRAYTAAAGADFP-----MDSNQC 170

QY 183 PAGGPFVCKCREPFPVPLIKESHPL---YNNKRTGOVNCAPCYO 223
Db 171 RGASSERCKCK---PIRATQKTYFRNNYVIRAKVKEIKTKCH 211

RESULT 6

US-08-878-474-7
Sequence 7, Application US/08878474
Patent No. 6133232

GENERAL INFORMATION:

APPLICANT: Boumeester, Lewis

APPLICANT: De Robertis, Edward M.

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

TITLE OF INVENTION: Factors

```

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/362-5418
TELEFAX: 415/248-5500
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-878-474-7

```

```

Query Match      28.0%; Score 367; DB 4; Length 323;
Best Local Similarity 35.8%; Pred. No. 7.3e-27;
Matches 77; Conservative 34; Mismatches 80; Indels 24; Gaps 6;

QY 14 LLLLAQLVGRRAAASKAPVCOEITVPMCGIGYNTLHMENQFNHDTODEAGLEVHOFMFL 73
DB 16 LVLALACLQVGAOAAACEPRIPPLCKSLPMNMKMPNHLHSTQANAILAMEOFBGL 75
QY 74 VEIOCSPLRFFLCTMYTPTICLPDY-HKRLPQRSVCERAKAGCSPLMRQYGFAMERMS 132
DB 76 LGTHCSPLDLFLCANYAICTIDFQHEPIKPKSVCEARAGQCEIILIKYHNSWESLA 135
QY 133 CRLPYLGDADVLCDVNRSEATTAPRRPFAKPTLPGPAGAPASGEGCPAGFPVCKC 192
DB 136 CDELPEYDGG---VCI--SPEAIVTADGADFP-----MDSSTGHCRCGASSEKCKC 180
QY 193 REPPVILKESHPL-----YNKVRTGQVPCAVPCY 223
DB 181 K---PVRATQKTYFRNNYNYVIRAKVKEVKMKCH 211

```

```

RESULT 7
US-08-878-474-3
Sequence 3, Application US/08878474
Patent No. 6133232
GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
APPLICANT: Boumeester, Lewis
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-878-474-3

```

```

Query Match      27.5%; Score 360; DB 4; Length 318;
Best Local Similarity 37.1%; Pred. No. 3.2e-26;
Matches 83; Conservative 34; Mismatches 73; Indels 34; Gaps 10;

QY 8 APPSLLLLLAQLVGRRAAASKAPVCOEITVPMCGIGYNTLHMENQFNHDTODEAGLEV 67
DB 14 AIPGLALLLP---NAVCAS---CEPVRIIPMCKSMWPMNMTKMPNHLHSTQANAILAI 65
QY 68 HOFPLVETIQSPDLRFLCTMYTPTICLPDY-HKRLPQRSVCERAKAGCSPLMRQYGF 126
DB 66 EGFEGILLTTECSQDLFLCANYAICTIDFQHEPIKPKSVCEARAGQCEIILIKYHT 125
QY 127 WEERMSCRLPYLGDADVLCDVNRSEATTAPRRPFAKPTLPGPAGAPASGEGCPAGG 186
DB 126 WESLACEELPYDGG---VCIS---PEAIVTVEQGTSMDF-----SMDSNNGKSGSR 175
QY 187 PFVCKREPFVPI-----LKESHPLYNKYRTGQVPCAVPCY 223
DB 176 EH-CKCK---PMKATQKTYLKN---YNYVIRAKVKEVKMKCH 211

```

```

RESULT 8
US-08-937-067-10
Sequence 10, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umaneky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067

```

FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
TELEFAX: (650) 813-5600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-10

Query Match 23.2%; Score 304.5; DB 4; Length 666;
Best Local Similarity 34.5%; Pred. No. 1.3e-20;
Matches 80; Conservative 27; Mismatches 76; Indels 49; Gaps 10;

QY 12 LLLALLQVGRRAAASAPVCOEITVPMCRGIGYNLTMPNQFNHDTODEAGLEVHOFW 71
DB 12 LLLVFLQIGHSIFS-----CEPITLMCODLPYNTTFMNLNHYDQOTPALAMEBFH 66
QY 72 PLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAGCSPLMRQYGFAMPERM 131
DB 67 PMVUDSDRDRPFLCALYATICH-EYGRVTLPCRRLCQRAYSECSKLMENFGVPMFPDM 125
QY 132 SCDBLPVLRDAEVLCDYNSSEATTAPRPPPAKPTLPGPP--GAPAS-----GGECPA 184
DB 126 ECSRFP-----DCD-----EPYRLVDNLVGDPTGAPVAVQORDGFWCP- 166
QY 185 GGPVCKCRFEFVFLKESHPL-YNKATGQYPCNAVCYCPSSADRTTA 235
DB 167 -----RE-----LKIDPLGYSL--HVRDCSPCPMRYRELSPA 202

RESULT 9
US-08-937-067-11
Sequence 11, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umanaky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-11

Query Match 22.9%; Score 299.5; DB 4; Length 537;
Best Local Similarity 34.1%; Pred. No. 3e-20;
Matches 59; Conservative 32; Mismatches 67; Indels 15; Gaps 4;

QY 14 LLLLAQVGRRAAASAPVCOEITVPMCRGIGYNLTMPNQFNHDTODEAGLEVHOFWPL 73
DB 28 LLLRLPLTGDEDEER--CDPIRIMCQNLGVVTKMPLVGHLELQTDALQLTTFTPL 85
QY 74 VEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAGCSPLMRQYGFAMPERMSC 133
DB 86 IOVCSQLOFFLCSYVPMCTEKINIPIGCGCMCLSVKRCSPVLRFEFGAMPDTLNC 145
QY 134 DRPLVLRDAEVLCDYNSSEATTAPRPPPAKPTLPGPPGAPASGGECPAGC 186
DB 146 SKRPP-QNDHNMCMESGDEEVPDPHKT-PIQP-----GGECHSVG 185

RESULT 10
US-08-987-289-2
Sequence 2, Application US/08987289
Patent No. 5994098
GENERAL INFORMATION:
APPLICANT: HU, ERDING
TITLE OF INVENTION: A Human 7-TM Receptor Similar
TITLE OF INVENTION: To Murine Fizzled-6 gene
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,289
FILING DATE: 09-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,725
FILING DATE: 02-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70060
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 946169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-987-289-2
Query Match 21.5%; Score 282; DB 2; Length 706;

Best Local Similarity 30.8%; Pred. No. 1.8e-18;
Matches 65; Conservative 22; Mismatches 80; Indels 44; Gaps 6;
QY 33 COEIVPCRGIGVYLTMPNOFNHDTODEAGLEVHGFVPLVEIOSPDLRFCTMTPT 92
Db 24 CEPTVPCMKKAYMTTFPMLMGHYDOSIAVEMHFLPLNMEHFLPTEFFLCKAVP 83
QY 93 ICLPDYHKPLPPECVSCERAKAGCSPLMRQYGFAMPBERMSCDLPLVLRDAEVLCDYNR 152
Db 84 TCIBGDIH-VVPRCKRLCEKVYSDCKLIDTFGIRWPELEECORLQYCEBTVPV----- 135
QY 153 SEATTAAPRRPF--PAKPTLPGPFGAPAGSGECPAGGPPVCKCRBEPVPLKESHPLYNKV 210
Db 136 ---TFDPHTEFGPKET-----EQYQDRIQFWC-----PRHLKT 167
QY 211 RTGQ-----VNCAPVCYQPSFSADERTFA 235
Db 168 SGGGQYKFLGIDQCAPPCPMYFKSDELEFA 198

RESULT 11

US-08-937-067-2

Sequence 2, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-937-067-2

Query Match 21.3%; Score 278.5; DB 4; Length 295;

Best Local Similarity 36.2%; Pred. No. 1.3e-18;

Matches 63; Conservative 27; Mismatches 61; Indels 23; Gaps 7;

QY 6 PSAPSLILLIAQ-----LVGRAAASAPVCOEI--TVMCRGIGVYLTMP 52

Db 2 PRGPASILLILVLASHCIGSARGLFLFGOPDRSYKTNCKPIPAVLQCHGIEYQNMRLP 61

QY 53 NQFNHDTODEAGLEVHGFVPLVEIOSPDLRFCTMTPTCLPDYHKPLPPECVSCER 111

Db 62 NLGHEITWKEY-LEQAGAMITLVMKQCHPDTKFLCSFAFVCLDDLDDETIQPCHSCLQV 120

QY 112 AKAGCSPLMRQYGFAMPBERMSCDLPLVLRDAEVLCDYNRSE---ATTAPR 161
Db 121 VKDCAPFMSAFGPWPDMLECDRFP---QDND-LCLPLASSDHLPLATEAPK 170

RESULT 12

US-08-937-067-12

Sequence 12, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 709 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-937-067-12

Query Match 20.7%; Score 271; DB 4; Length 709;

Best Local Similarity 30.6%; Pred. No. 2e-17;

Matches 71; Conservative 22; Mismatches 95; Indels 44; Gaps 8;

QY 10 PSILLILIAQLVGRAAASAPVCOEITVPMCRGIGVYLTMPNOFNHDTODEAGLEVH 69

Db 5 PELLACILLPLV---RGHSIFTECEPITVPCMKMTVMNMTFFPMLMGHYDOSIAVEMH 60

QY 70 FWPVLEIOSPDLRFCTMTPTCLPDYHKPLPPECVSCERAKAGCSPLMRQYGFAMP 129

Db 61 FLHLANLSCSPNIMFICQAFIPTCTQIHVYL-PCKRLCEKIVSDCKLMDTFGIMPE 119

QY 130 RMSCDRLPVLGRDAEVLCDYNRSEATTAPRPPAKPTLPGPAGAPAGSGECPAGSPFV 189

Db 120 ELECNRLP-----HCDD-----TVPVTSHP-HTELSGF---QKSDQVPRDIGFW 160

QY 190 CKCREPVPVPLIKESHPLYNKYRTGQ-----VNCAPVCYQPSFSADERTFA 235

Db 161 C-----PKHLRPSDQGYRFLGIEQCAPPCPMYFKSDELEFA 198

RESULT 13

US-08-937-067-4

Sequence 4, Application US/08937067


```

Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umaneky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-4

```

Query Match 20.6%; Score 270; DB 4; Length 212;

Best Local Similarity 31.3%; Pred. No. 5.6e-18; Matches 73; Conservative 27; Mismatches 81; Indels 52; Gaps 10;

```

QY 9 PPSLLLLLAQ-----LVGRAAASAKAVCOEI--TVMCRGIGYNLTHMPNOF 55
DB 5 PPSLLFLFLASHCCLGSRGLFLFGQPDFSYKSNCKRIPANLQCHIEYQNMRLPVL 64
QY 56 NHTQDEAGLEVHOFM-PLVEIQSPDLRFLCTMYTPICLPDYHKPLPGRSVCEAKA 114
DB 65 GHETMKEV-LEQAGAWIPLVKQCHPDKFKLCSLFAVCLDDDETQPCSHXCVCVKD 123
QY 115 GCSPLMROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPKPLPGPFG 174
DB 124 RCAVWNAFAGFPWDMLECDRFP--QDND-LCTPLASSD-----HLLPATEE 167
QY 175 APASGEGCPAGPFVCK-----CRPEFVPLIKESHPLYNKVTGQ 214
DB 168 APK---VCEA-----CKWKNDNDNDIMETLCKNDPALKIKYKEITYINRRGR 212

```

RESULT 14
US-08-937-067-6

Sequence 6, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umaneky, Samuil

APPLICANT: Melkonian, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

```

STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-6

```

Query Match 20.6%; Score 270; DB 4; Length 317;

Best Local Similarity 38.2%; Pred. No. 9.2e-18; Matches 52; Conservative 24; Mismatches 50; Indels 10; Gaps 5;

```

QY 28 SKAVCOEI--TVMCRGIGYNLTHMPNOFNHTQDEAGLEVHOFPLVLIQSPDLRF 85
DB 48 SKPEQCDIPADLPCTVTKYKMRPLNLEHSLAEVKKQASSWPLLAKRCHSDTQVF 107
QY 86 LCTWYTPICLPDYHKPLPGRSVCEAKACSPLMROYGFAMPERMSCDRLPVLGRDAEV 145
DB 108 LCSLFAVCL---DRPIYPRSLCEAVRACAPLMEAYGFPMWMLHCHKFP-LDND--- 160
QY 146 LCMYDNRSE-ATTAP 160
DB 161 LCIAVCGHLPATAP 176

```

RESULT 15
US-08-937-654B-6

Sequence 6, Application US/0893654B

Patent No. 6165748

GENERAL INFORMATION:

APPLICANT: RACIE, LISA, ET ALIA

TITLE OF INVENTION: FRAZZLED NUCLEOTIDE SEQUENCES,

TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESSES:

ADDRESSEE: GENETICS INSTITUTE, INC.

STREET: 87 CAMBRIDGE PARK DRIVE

CITY: CAMBRIDGE

STATE: MA

COUNTRY: USA

ZIP: 02140-2387

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/893,654B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MEINERT, M.C.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:35:02 ; Search time 22 Seconds
(without alignments)
1030.270 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310 1 MARRPDSAPPSSLILLLLAQL.....PNCVPCYQPSFSADERTFA 235

Sequence: 1 MARRPDSAPPSSLILLLLAQL.....PNCVPCYQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

362588

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	235	9	US-09-847-102a-68
2	1310	100.0	585	9	US-10-146-474-9
3	1310	100.0	585	9	US-09-847-102a-51
4	1310	100.0	586	9	US-10-152-548-10
5	1111	84.8	516	9	US-09-847-102a-38
6	824	62.9	277	9	US-09-847-102a-76
7	824	62.9	694	9	US-09-847-102a-53
8	823.5	62.9	274	9	US-09-847-102a-74
9	823.5	62.9	682	9	US-10-152-548-16
10	823.5	62.9	685	9	US-10-146-474-14
11	823.5	62.9	685	9	US-09-847-102a-57
12	740.5	56.5	599	9	US-09-847-102a-37
13	621	47.4	694	9	US-10-152-548-2
14	585	44.7	570	9	US-09-847-102a-43
15	477	36.4	244	9	US-09-847-102a-63
16	477	36.4	565	9	US-10-146-474-8
17	477	36.4	565	9	US-09-847-102a-46
18	461	35.2	253	9	US-09-847-102a-71
19	461	35.2	574	9	US-09-847-102a-54

20	440.5	33.6	251	9	US-09-847-102a-72	Sequence 72, Appl
21	440.5	33.6	572	9	US-10-146-474-13	Sequence 13, Appl
22	440.5	33.6	572	9	US-09-847-102a-55	Sequence 55, Appl
23	440.5	33.6	573	9	US-10-152-548-14	Sequence 14, Appl
24	424	32.4	529	9	US-09-847-102a-41	Sequence 41, Appl
25	422	32.2	214	9	US-09-847-102a-62	Sequence 62, Appl
26	422	32.2	626	9	US-09-847-102a-45	Sequence 45, Appl
27	415	31.7	319	9	US-09-847-102a-61	Sequence 61, Appl
28	415	31.7	647	9	US-09-847-102a-75	Sequence 75, Appl
29	394.5	30.1	231	9	US-09-847-102a-75	Sequence 75, Appl
30	394.5	30.1	232	9	US-09-847-102a-75	Sequence 75, Appl
31	394.5	30.1	591	9	US-09-847-102a-58	Sequence 58, Appl
32	394	30.1	591	9	US-09-847-102a-59	Sequence 59, Appl
33	384	29.3	227	9	US-09-847-102a-77	Sequence 77, Appl
34	384	29.3	581	9	US-09-847-102a-60	Sequence 60, Appl
35	380.5	29.0	543	9	US-09-847-102a-39	Sequence 39, Appl
36	378	28.9	544	9	US-09-847-102a-40	Sequence 40, Appl
37	372	28.4	325	9	US-09-803-170C-9	Sequence 9, Appl
38	372	28.4	325	9	US-09-974-298-17	Sequence 17, Appl
39	372	28.4	325	9	US-10-090-049-4	Sequence 4, Appl
40	372	28.4	325	10	US-09-903-180B-9	Sequence 9, Appl
41	372	28.4	325	10	US-09-903-187A-9	Sequence 9, Appl
42	372	28.4	325	10	US-09-903-171A-9	Sequence 9, Appl
43	372	28.4	325	10	US-09-903-188A-9	Sequence 9, Appl
44	372	28.4	325	10	US-09-903-325A-9	Sequence 9, Appl
45	372	28.4	325	10	US-09-903-325A-9	Sequence 9, Appl

ALIGNMENTS

```
RESULT 1
US-09-847-102a-68
; Sequence 68, Application US/09847102A
; Publication NO. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripac
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leonil M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102a-68

Query Match 100.0% Score 1310; DB 9; Length 235;
Best Local Similarity 100.0% Pred No. 1e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRPDSAPPSSLILLLLAQLVGRRAAASKAPVCOEITVPCRGIGVNLTHMPQFNHDTQ 60
Db 1 MARRPDSAPPSSLILLLLAQLVGRRAAASKAPVCOEITVPCRGIGVNLTHMPQFNHDTQ 60
QY 61 DEAGLEVHQWPLVEIQCSDFLRFICTWTPTICLDYHNPPLPCRSVCRAAAGSPLM 120
Db 61 DEAGLEVHQWPLVEIQCSDFLRFICTWTPTICLDYHNPPLPCRSVCRAAAGSPLM 120
QY 121 ROYGFAMPEMSSCDRLPVLCGRDAEVLICMDYRSEATTAAPPAPPAKPTLPGPAPASGG 180
Db 121 ROYGFAMPEMSSCDRLPVLCGRDAEVLICMDYRSEATTAAPPAPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKEPEVPVILIKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235
Db 181 ECPAGGFVCKEPEVPVILIKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235
```

Db 181 ECPAGGFVCKRPFVILKESHPLYNKVRTGQVNCVPCYOPSFADERTFA 235

RESULT 2

US-10-146-474-9
; Sequence 9, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Umaneky, Samuil
; Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & ROEBSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,474
; FILING DATE: 14-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-146-474-9

Query Match 100.0%; Score 1310; DB 9; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.7e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPSPAPSLILLILALQVGRAAASKAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQ 60
Db 1 MARPPSPAPSLILLILALQVGRAAASKAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQ 60
QY 61 DEAGLEVHQFMPVLEIQCSDDLRFELCTMTYTPICLPDYHKPLPPCRSVCCERAKGCSPLM 120
Db 61 DEAGLEVHQFMPVLEIQCSDDLRFELCTMTYTPICLPDYHKPLPPCRSVCCERAKGCSPLM 120
QY 121 ROYGFAMPERNMSCRLPVLGRDAEVLCDYNRSEATTAPPRPFAKPTLPGPGAPASGG 180
Db 121 ROYGFAMPERNMSCRLPVLGRDAEVLCDYNRSEATTAPPRPFAKPTLPGPGAPASGG 180
QY 181 ECPAGGFVCKRPFVILKESHPLYNKVRTGQVNCVPCYOPSFADERTFA 235
Db 181 ECPAGGFVCKRPFVILKESHPLYNKVRTGQVNCVPCYOPSFADERTFA 235

RESULT 3
US-09-847-102A-51

; Sequence 51, Application US/09847102A
; Publication No. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Cort, Maripac
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leon M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq. for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-51

Query Match 100.0%; Score 1310; DB 9; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.7e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPSPAPSLILLILALQVGRAAASKAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQ 60
Db 1 MARPPSPAPSLILLILALQVGRAAASKAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQ 60
QY 61 DEAGLEVHQFMPVLEIQCSDDLRFELCTMTYTPICLPDYHKPLPPCRSVCCERAKGCSPLM 120
Db 61 DEAGLEVHQFMPVLEIQCSDDLRFELCTMTYTPICLPDYHKPLPPCRSVCCERAKGCSPLM 120
QY 121 ROYGFAMPERNMSCRLPVLGRDAEVLCDYNRSEATTAPPRPFAKPTLPGPGAPASGG 180
Db 121 ROYGFAMPERNMSCRLPVLGRDAEVLCDYNRSEATTAPPRPFAKPTLPGPGAPASGG 180
QY 181 ECPAGGFVCKRPFVILKESHPLYNKVRTGQVNCVPCYOPSFADERTFA 235
Db 181 ECPAGGFVCKRPFVILKESHPLYNKVRTGQVNCVPCYOPSFADERTFA 235

RESULT 4
US-10-152-548-10
; Sequence 10, Application US/10152548
; Publication No. US20030040051A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Purnima
; Brink, Marcel
; Harryman, Cindy S.
; Wang, Yanshu
; Hsieh, Jen-chih
; Andrew, Deborah
; Nathans, Jeremy
; Nusse, Roel

; TITLE OF INVENTION: Wnt Receptor Compositions and Methods
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/152,548
; FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hf55 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-152-548-10

Query Match 100.0%; Score 1310; DB 9; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,7e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARDPSPAPSLLLLLLAQLVGRRAAASKAAPVCOEITVPMCRGIGYVLTMPNPFNDTQ 60
DB 1 MARDPSPAPSLLLLLLAQLVGRRAAASKAAPVCOEITVPMCRGIGYVLTMPNPFNDTQ 60
QY 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
DB 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPAPKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKREPFVILKESHPLYNKVTGQVNCAPVCYOPSFSADERTFA 235
DB 181 ECPAGGFVCKREPFVILKESHPLYNKVTGQVNCAPVCYOPSFSADERTFA 235

RESULT 5
US-09-847-102A-38
; Sequence 38, Application US/09847102A
; Publication No. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leoni M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-38

Query Match 84.8%; Score 1111; DB 9; Length 516;

Best Local Similarity 87.2%; Pred. No. 2.1e-81;
Matches 205; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
QY 1 MARDPSPAPSLLLLLLAQLVGRRAAASKAAPVCOEITVPMCRGIGYVLTMPNPFNDTQ 60
DB 1 MARDPSPAPSLLLLLLAQLVGRRAAASKAAPVCOEITVPMCRGIGYVLTMPNPFNDTQ 60
QY 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
DB 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPAPKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKREPFVILKESHPLYNKVTGQVNCAPVCYOPSFSADERTFA 235
DB 181 ECPAGGFVCKREPFVILKESHPLYNKVTGQVNCAPVCYOPSFSADERTFA 205

RESULT 6
US-09-847-102A-73
; Sequence 73, Application US/09847102A
; Publication No. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leoni M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-73
Query Match 62.9%; Score 824; DB 9; Length 277;
Best Local Similarity 59.9%; Pred. No. 1.1e-58;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
QY 11 SLT--LLLLLAQLVGRRAAASKAAPVCOEITVPMCRGIGYVLTMPNPFNDTQDEAGLEVH 68
DB 11 SLTAAALLLORSSGAASAKELACQETITVPLCKGICYNVITMPNPFNDTQDEAGLEVH 70
QY 69 QFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLMROYGFAWP 128
DB 71 QFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLMROYGFAWP 130
QY 129 ERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPAPKPTLPGPAPASGG 174
DB 131 DRMKCDRLPVG--NPTDLCMDYNRSEATTAPPPAPKPTLPGPAPASGG 187
QY 175 A-----PASGG-----ECPAGGFV-----CKREFVPLKESH 205
DB 188 ARPHRGGGCGGGGAAAPARAGGGGGAARPPGGGAACEFCGCRARAVSVSSRRH 247
QY 206 LYNKVTGQVNCAPVCYOPSFSADERTFA 234
DB 248 LYNKVTGQVNCAPVCYOPSFSADERTFA 276
RESULT 7
US-09-847-102A-56
; Sequence 56, Application US/09847102A
; Publication No. US20030044409A1

```

: GENERAL INFORMATION:
: APPLICANT: University of California
: APPLICANT: Carson, Dennis A.
: APPLICANT: Corr, Maripat
: APPLICANT: Rhee, Chae-Seo
: APPLICANT: Lorenzo, Leonl M.
: APPLICANT: Malini, Sen
: TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
: TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
: FILE REFERENCE: 22000-20659 .00
: CURRENT APPLICATION NUMBER: US/09/847.102A
: CURRENT FILING DATE: 2001-05-01
: NUMBER OF SEQ ID NOS: 138
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 56
: LENGTH: 694
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-847-102A-56

```

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: M28 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16;
US-10-152-548-16

Query Match 62.9%; Score 823.5; DB 9; Length 682;
Best Local Similarity 60.0%; Pred. No. 3e-58;

Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

QY 11 SLT-LLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQHDTODEAGLEVH 68
DB 11 SLTAAVLQRSSGAASAASAKELACQETIVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 128
DB 71 QFWPLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLGRDAEVLCDVYRSEATTA---PRRFPKPTLPG-----PRG 174
DB 131 DRMKCDRLPEQG-NPDTLCMDYNTDITTAAPSPRRLLPPPP-PGEQPPSGSGHSRPPG 188
QY 175 A-----PASGSEC--PAGGPFV---CKREPFVPLIKESHPLYNK 209
DB 189 ARPHRGSSRGSGDAAPSPSRGKARPPGGAAPCEPCQCCTAPMVSVSSEHPLYNR 248
QY 210 VRTGVNCAVPCYQPSFSADERTF 234
DB 249 VKTQIANCALPCHNPFPSQDERAF 273

RESULT 10

US-10-146-474-14
Sequence 14, Application US/10146474
Publication No. US20030023061A1

GENERAL INFORMATION:

APPLICANT: Umanaky, Samuel

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/146,474

FILING DATE: 14-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 685 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 14;
US-10-146-474-14

Query Match 62.9%; Score 823.5; DB 9; Length 685;
Best Local Similarity 60.0%; Pred. No. 3e-58;

Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

QY 11 SLT-LLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQHDTODEAGLEVH 68
DB 11 SLTAAVLQRSSGAASAASAKELACQETIVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 128
DB 71 QFWPLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLGRDAEVLCDVYRSEATTA---PRRFPKPTLPG-----PRG 174
DB 131 DRMKCDRLPEQG-NPDTLCMDYNTDITTAAPSPRRLLPPPP-PGEQPPSGSGHSRPPG 188
QY 175 A-----PASGSEC--PAGGPFV---CKREPFVPLIKESHPLYNK 209
DB 189 ARPHRGSSRGSGDAAPSPSRGKARPPGGAAPCEPCQCCTAPMVSVSSEHPLYNR 248
QY 210 VRTGVNCAVPCYQPSFSADERTF 234
DB 249 VKTQIANCALPCHNPFPSQDERAF 273

RESULT 11

US-09-847-102a-57
Sequence 57, Application US/09847102A
Publication No. US2003004409A1

GENERAL INFORMATION:

APPLICANT: University of California

APPLICANT: Carson, Dennis A.

APPLICANT: Corr, Maripat

APPLICANT: Rhee, Chae-Seo

APPLICANT: Lorenzo, Leonl M.

APPLICANT: Melini, Sen

TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR

STUDYING AND TREATING CANCERS EXPRESSING PRIZZLED ANTIGENS

FILE REFERENCE: 22000-20629.00

CURRENT APPLICATION NUMBER: US/09/847,102A

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 57

LENGTH: 685

TYPE: PRT

ORGANISM: Mouse

US-09-847-102a-57

Query Match 62.9%; Score 823.5; DB 9; Length 685;

Best Local Similarity 60.0%; Pred. No. 3e-58;

Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

QY 11 SLT-LLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQHDTODEAGLEVH 68
DB 11 SLTAAVLQRSSGAASAASAKELACQETIVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 128
DB 71 QFWPLVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLGRDAEVLCDVYRSEATTA---PRRFPKPTLPG-----PRG 174
DB 131 DRMKCDRLPEQG-NPDTLCMDYNTDITTAAPSPRRLLPPPP-PGEQPPSGSGHSRPPG 188
QY 175 A-----PASGSEC--PAGGPFV---CKREPFVPLIKESHPLYNK 209
DB 189 ARPHRGSSRGSGDAAPSPSRGKARPPGGAAPCEPCQCCTAPMVSVSSEHPLYNR 248

QY 210 VRTGVNCAVPCYQPSFSADERTF 234
Db 249 VKTGIANCALPCHNPFPSQDERAF 273

RESULT 12

US-09-847-102A-37
Sequence 37, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Cort, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leoni M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629-00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 599
TYPE: PRT
ORGANISM: Mouse
US-09-847-102A-37

Query Match 56.5%; Score 740.5; DB 9; Length 599;
Best Local Similarity 60.3%; Pred. No. 1.2e-51;
Matches 146; Conservative 20; Mismatches 43; Indels 33; Gaps 7;

QY 11 SLL--LILLAQVGRGAASAKAPVCOEITVPMCRGIGYNTLTHMPNQHNDODEAGLEVH 68
Db 11 SLLAALAVLQRRSGAASAKELACOEITVPLCKGIGYNTLTHMPNQHNDODEAGLEVH 70
QY 69 QFWPLVEIQCSFDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 128
Db 71 QFWPLVEIQCSFDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 130
QY 129 ERMSCDRLPVLRDAEVLICMDYNRSEATTA--PPRPPAKTLPD-----PPG 174
Db 131 DMRRCDBRLPEQG-NPDTLCMDYNRDTLTTAAPSPPRLPPPP-PPGPPSGSGSRPPG 188
QY 175 A--PASGGECPAGGFVCKEPPFPIKESHPLNKNKRTGVNCAVPCYQPSFSADERTF 232
Db 189 APPRGGSSRSGD-----AAAAPPSSGGGTGIANCALPCHNPFPSQDERAF 235
QY 233 TF 234
Db 236 AF 237

RESULT 13

US-10-152-548-2
Sequence 2, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Heileh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy
APPLICANT: Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/152,548

FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/832,340

FILING DATE: 11-APR-1997

APPLICATION NUMBER: US 60/015,307

FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8600-0167.30

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 694 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Dfz2 Polypeptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-152-548-2

Query Match 47.4%; Score 621; DB 9; Length 694;

Best Local Similarity 43.4%; Pred. No. 5.1e-42; Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY 22 GRAAASAP-----VCOEITVPMCRGIGYNTLTHMPNQHNDODEAGLEVH 68
Db 40 GHGADAPAPGYVAPLPKDNELRCEIITIPMCRGIGYNTSFPENKWHETODEAGLEVH 99
QY 69 QFWPLVEIQCSFDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 128
Db 100 QFWPLVEIQCSFDLRFPLCTMYTPICLPDYHKPLPPCRSVCEKAKAGCSPLMROYGFAMP 159
QY 129 ERMSCDRLPVLRDAEVLICMDY----- 150
Db 160 ERMSCEHPLHG-DPDTLCMEQPSYTEAGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGS 218
QY 151 ---NRSEATTAPRPPAKTLPDPPGAPASGGECPAGGFVCKEPPV----- 197
Db 219 GAGSGSGSTSTKPCRGRNSK-NQNPQGEKASGKEG-----CSGRSPLIFLCKEQLQ 271
QY 198 -----PIKESHPLYNKV---RTGVNCAVPCYQPSFSADERTF 235
Db 272 QOSQPMWHHPHWYNNLTVQRIAGVNCGLPKCGPFPSSDEKDF 317

RESULT 14

US-09-847-102A-43
Sequence 43, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Cort, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leoni M.

APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 570
TYPE: PRF
ORGANISM: Drosophila
US-09-847-102A-43

Query Match 44.7%; Score 585; DB 9; Length 570;
Best Local Similarity 48.3%; Pred. No. 3,2e-39;

Matches 117; Conservative 25; Mismatches 52; Indels 48; Gaps 6;

QY 22 GRAAASAP-----VCOETVPMCRGIGYLTMPNQFNHDTQDEAGLEVH 68
DB 29 GHGLDASBPAGYVPAIPKDPNLRCBITIPMCRGIGYNTSPFNEMNHETQDEAGLEVH 88
QY 69 QFWPLVETIQSPDLRFPLCTMTYTPICLPDYHKPLPCRSVCERAKAGCSPLMRQYGFAMP 128
DB 89 QFWPLVETIKSPDLKFLCSMTYTPICLEDYHKPLPVCRSVCERARSGCAPIMQYSEFWP 148
QY 129 ERMSCDRLPVGRDAEVLCDY-NRSEATTAAPPAPKPTLPGPAPASG----- 179
DB 149 ERMACENLPLHG-DPDLNLCMEQPSYTEAGSGS-----SGSGSGSGSGSGSGGKRRK 198
QY 180 -----GECRAGPFCVCKRBPVILKESHPLYNKVTGQVPCAVPCYQPSFADERT 233
DB 199 QGSGSGSGSGSGSGS-----TSTKPCRGQRGIAGVPCGIPCKGPPFSNDEKD 248
QY 234 FA 235
DB 249 FA 250

RESULT 15

US-09-847-102A-63
Sequence 63, Application US/09847102A
Publication No. US2003004409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Cort, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leonil M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 244
TYPE: PRF
ORGANISM: Homo sapiens
US-09-847-102A-63

Query Match 36.4%; Score 477; DB 9; Length 244;
Best Local Similarity 41.9%; Pred. No. 5.8e-31;

Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RPDSPAPPSLLILLIAQLVGRRAAASAPV-----COETVPMCRGIGYLTMPNQF 55
DB 2 RPRSALEPLLLPLLLPAGAPAGQFHGKGISIPDHGFCQIPISIPCTDIAYNOTIMPVL 61
QY 56 NHTQDEAGLEVHOFWPLVETIQSPDLRFPLCTMTYTPICLPDYHKPLPCRSVCERAKAG 115

DB 62 GHTNQEDAGLEVHOFYPLVKVQCSPEILRFLLCSMYAVCTV-LEQAIIPCRSICERAROG 120
QY 116 CSPLMROYGFAMPERMSCDRLPVGRDAEVLCDYNRSE-----ATTAPRPFPFA-KPT 168
DB 121 CEALMKNKFGQWPERLACEHFPNKG--AEQICVQNHSEDOGAPALLTTAP---PGLQPG 175
QY 169 LPGPAPASGSECPAGG---PFVCKRBPVILKESHPLYNKVTGQVPCAVPCYQ 224
DB 176 AGTPGPGPGGGAAPPYATLEHPPHCP-----RVLKV--PSYLSYKFLGBRDCAPC-E 226
QY 225 PS-----FSADERTFA 235
DB 227 PARPDGSMFFSOETRFA 244

Search completed: May 19, 2003, 16:43:39
Job time : 25 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using SW model

Run on: May 19, 2003, 16:32:41 ; Search time 20 Seconds

(without alignments)
1129.579 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARPDSPAPSLLLLLLAQL.....PNCAPVCYQSPFSADERTFA 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	621	47.4	694	2	Wingless receptor
2	477	36.4	565	2	Fritzzled-2 protein
3	461	35.2	574	2	Fritzzled-7 protein
4	451	34.4	550	2	Wingless protein x
5	415	31.7	647	2	Fritzzled-1 protein
6	399	30.5	641	2	Probable intercell
7	384	29.3	581	2	FZD10 protein - hu
8	370.5	28.3	581	2	gene fritzzled prot
9	366.5	28.0	605	2	hypothetical prote
10	339.5	25.9	568	2	Fritzzled-1 protein
11	334	25.5	197	2	Fritzzled-related p
12	308	23.5	537	2	Fritzzled protein 4
13	297	22.7	666	2	Fritzzled-3 protein
14	282	21.5	706	2	Fritzzled-6 protein
15	270.5	20.6	295	2	Fritzzled protein-2
16	270	20.6	317	2	Fritzzled protein-1
17	218.5	16.7	1113	2	low-density lipopr
18	170	13.0	579	2	membrane-type friz
19	161.5	12.3	526	2	Fritzzled protein h
20	140.5	10.7	1774	2	collagen alpha 1(X
21	127.5	9.7	793	2	Smoothed protein
22	106.5	8.1	1955	1	agrin precursor -
23	98.5	7.5	768	2	protein ZC123.1 (I
24	96.5	7.4	211	2	protein F45B8.3 (I
25	96.5	7.4	241	2	hypothetical prote
26	95	7.3	1428	2	luerin A - Calif
27	94.5	7.2	347	2	hypothetical prote
28	93	7.1	871	1	protein-tyrosine k
29	93	7.1	881	1	protein-tyrosine k

30	93	7.1	1464	2	SS9856	collagen alpha 1(I
31	92.5	7.1	494	2	A42170	zinc finger protei
32	92	7.0	1464	1	CGHUS	collagen alpha 1(I
33	91.5	7.0	303	2	T28999	hypothetical prote
34	90	6.9	488	2	A27153	collagen alpha 1(I
35	90	6.9	1221	2	A49457	fibulin-2 precursor
36	89.5	6.8	674	2	S13301	collagen alpha 1(X
37	88.5	6.8	196	2	A48150	hibernation-relate
38	88.5	6.8	316	2	T31880	hypothetical prote
39	88	6.7	215	2	B48150	hibernation-relate
40	87.5	6.7	375	2	T16248	hypothetical prote
41	87.5	6.7	396	1	KXBOZ	plasma protein 2 -
42	87	6.6	510	1	S43692	transcription fact
43	86.5	6.6	346	2	T01123	hypothetical prote
44	86.5	6.6	700	2	D75508	serine/threonine p
45	86	6.6	289	2	S55667	thymidylate synth

ALIGNMENTS

RESULT 1

Wingless receptor precursor dfz2 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Mar-2001
C:Accession: S71786; S78444

R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macne, J.P.; Andrew, Nature 382, 225-230, 1996
A:Title: A new member of the fritzzled family from *Drosophila* functions as a wingless rec

A:Reference number: S71786; MUID:96353971; PMID:8717036
A:Accession: S71786

A:Molecule type: DNA
A:Status: nucleic acid sequence not shown

A:Residues: 1-694 <BHA>

A:Cross-references: EMBL:U65589
A:Note: mRNA was also sequenced

R:Bhanot, P.; Wang, Y.; Nathans, J.
submitted to the EMBL Data Library, July 1996

A:Reference number: S78444
A:Accession: S78444

A:Molecule type: DNA
A:Residues: 1-416, 'T', 418-694 <BMW>

A:Cross-references: EMBL:U65589; NID:G1518050; PIDN:AC427273.1; PID:G1518051
C:Genetics:

A:Gene: dfz2
A:Cross-references: FlyBase:FBgn0016797
C:Superfamily: Fruit fly fritzzled protein

C:Keywords: transmembrane protein

Query Match 47.4% Score 621; DB 2; Length 694;
Best Local Similarity 43.4% Pred. No. 6.6e-42;
Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY	22	GRAAASKAP-----VCQEITVPMCRSIGVNLTMPPNQFNHDTODEAGLEVN	68
DB	40	GGGLDASPAHGVGVAIRPDPLRCEBITIPWCRIGVNMISFPMNMHETDEAGLEVN	99
QY	69	QFWPLVEIQCSPLDRPFLCTMYTPICLPDYHKLPPPCSVCCRAVAGSGPLMRQYGFAMP	128
DB	100	QWPLVEIKCSPLDRPFLCTMYTPICLPDYHKLPPPCSVCCRAVAGSGPLMRQYGFAMP	159
QY	129	ERMSCDRLPVGRDVEVCMQV-----	150
DB	160	ERMSCDRLPVGRDVEVCMQV-----	218
QY	151	NRSEATTAPRRFPFAKPTLPAPGAPASGECPPAGGPFVCKCRBEFV-----	197
DB	219	GAGSSGSGTSTPCRCGRMSK-NQNPQGEKASGKES-----GSCRSPILITLGEKQLQ	271
QY	198	PIKESHPLYNKY---RTGOVNCAPVCYQSPFSADERTFA 235	
DB	272	QOSQPMHMHPRHMYMNLTVQRIAGVPNCGIPCKGPFFSNDKDPFA 317	

RESULT 2

Frizzled-2 protein - human

C:Species: Homo sapiens (man)

C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001

C:Accession: J03038

R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 252, 117-122, 1998

A:Title: Molecular cloning, differential expression, and chromosomal localization of human

A:Reference number: J03037; PMID:99032814; PMID:9813155

A:Accession: J03038

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-565 <SAG>

A:Cross-references: DDBJ:AB017364; NID:93927884; PIDN:BA34667.1; PID:93927885

C:Superfamily: fruit fly frizzled protein

Query Match

36.4%; Score 477; DB 2; Length 565;

Best Local Similarity 41.9%; Pred. No. 1.5e-30;

Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RPPSPAPSLILLILLIAQLVGRAAAASAPV-----COEITVPMCKGIGYNTLTMNQF 55

DB 2 RPPSAPRLPLPLPLPMAAPQAFHGEKGISDPHGFQCPISIPLCIDIAVNOTIMENL 61

QY 56 NHDTODAGLEVHOFWFLVEIQCSPDLRFPLCTMYTPICLPDYHKPLPCRVCERAKAG 115

DB 62 GHTNQGEGLEVHOFVPLVAVQSPDLRFPLCTMYTPICLPDYHKPLPCRVCERAKAG 120

QY 116 CSPLMROYGFAWPERMSCDRLPVLGRDAEVLCDYNNSE-----ATTAPRPFPRA-KPT 168

DB 121 CEALNMKFGQWPERLRCEHFRPHG--AEQICVGNHSEEDGAPALLTAPR---PGLQPG 175

QY 169 LPPPGAPASGGECPAG---PPVCKCRFPFPIKESHPLNKKVKTGOVPCAVPCYO 224

DB 176 AGCTPGGPGGGGAPPRVATLEHFFHCP-----RLKLV--PSYLSYKFLGERDCAAPC-E 226

QY 225 PS-----PSADERTPA 235

DB 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

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QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 105 C8SVCEKAVAGCSPLMROYGFAWPERMSCDRLPVLGRDAEVLCDYNNSEATTAP---PR 161

DB 120 C8SLICERAROGCEALMKNKGFQWPERLRCEHFRPHG--AGEICVGNHSEEDGAPALLTAPR---PGLQPG 177

QY 162 PFPAPKPTLPG-----PPGAPASGGECPAGGPFVCKCRFPFPIKESHPLNKKVKTGOV 215

DB 178 APTATYLDLPPTLPPG--ASDGGPAPFPSPC-RQLKVP-----PYIGYRPLGE- 227

QY 216 PNCVAPCYOPS-----PSADERTPA 235

DB 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

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QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

QY 228 RDGAGC-EPGRANGLMYKEERRRA 253

Matches 104; Conservative 30; Mismatches 87; Indels 68; Gaps 11;

QY 3 RP--DPSAPPSTLLLL-----AQLVG-PAASAASKAP----- 31

DB 43 RPPVDRRLARQLLLMLLEAPLLGLVRAQAAGGPGGCGQPPPPPPQOQSGQY 102

QY 32 -----VCEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHQFWPLVEIQCS 79

DB 103 NGERGISVDPDHGQCPISIPDLCTDIAYNOTIMENLLGHTNQEDAGLEVHQFWPLVQVCS 162

QY 80 PDLRFLCTMYTPICLPDHHKPLPCRSVCERAKAGCSPLMRQYGFAMPBMSCDRLPYL 139

DB 163 AEKFKFLCSNYAVCTV-LEQALPPCRSLCERARQGCBAALMNKFGQWPDTLKCEKFPYA 221

QY 140 GRDAEVLCDMDYNSSEATTAPRPPFPKPTLPGPAGAPASGCECPAG-----GPFVCKCR 193

DB 222 G--AGSLCTGQONTSDKGTPTPISLLPFWMTSNPQHGGGHRGFGPGAGASERKFCSP-R 278

QY 194 EPPVPLKESHPLYNKVRITGVNCAVPCYOPS-----FSADERTFA 235

DB 279 ALKVPYLYNVHFLGKER-----DCGAPC-EPTKYVGLMYFGPEELRFS 319

RESULT 6

A45054

probable intercellular signal transducer or transmitter Fz-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001

C:Accession: A45054

R:Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, J. Biol. Chem. 267, 25202-25207, 1992

A:Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed

A:Reference number: A45054; MUID:93094228; PMID:1334084

A:Accession: A45054

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-641 <CH>

A:Experimental source: UMR 106 osteosarcoma cell line

A>Note: sequence extracted from NCBI backbone (NCBI:P120154)

C:Superfamily: fruit fly frizzled protein

Query Match 30.5%; Score 399; DB 2; Length 641;

Best Local Similarity 40.7%; Pred. No. 2.8e-24;

Matches 88; Conservative 28; Mismatches 74; Indels 26; Gaps 8;

QY 33 COEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHQFWPLVEIQCSPLDRFLCTMYTP 92

DB 111 CQITISIPDLCTDIAYNOTIMENLLGHTNQEDAGLEVHQFWPLVQVCSAEKFKFLCSMYAP 170

QY 93 ICLPDYHKLPPCRSVCEKAKAGCSPLMRQYGFAMPBMSCDRLPYLGRDAEVLCDMDYNR 152

DB 171 VCTV-LEQALPPCRSLCERARQGCBAALMNKFGQWPDTLKCEKFPVHGRE--LCGQNT 226

QY 153 SEATTAPRPPFPKPTLPGPAGAPASGCECPAG-----GPFVCKCRPPVPLKESHPL 206

DB 227 SDKGTPTPISLLPFWMTSNPQHGGGHRGFGPGAGASERKFCSP-RALRVPYLYNVHFL 285

QY 207 YNKVRITGVNCAVPCYOPS-----FSADERTFA 235

DB 286 GAK-----DCGAPC-EPTKYVGLMYFGPEELRFS 313

RESULT 7

JCT086

FZD10 protein - human

C:Species: Homo sapiens (man)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001

C:Accession: JCT086

R:Koike, J.; Takagi, A.; Miwa, T.; Hirai, M.; Terada, M.; Katoh, M. Biochem. Biophys. Res. Commun. 262, 39-43, 1999

A:Title: Molecular cloning of Frizzled-10, a novel member of the Frizzled gene family.

A:Reference number: JCT086; MUID:93982237; PMID:10448064

A:Accession: JCT086

A:Molecule type: mRNA

A:Residues: 1-581 <KO>

A:Cross-references: DDBJ:AB027464; NID:95834487; PIDN:BA84093.1; PID:95834488

A:Experimental source: fetal lung

C:Genetics:

A:Gene: Frizzled-10 (fzd-10)

A:Map position: 12q24.33

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein; lung; transmembrane protein

Query Match 29.3%; Score 384; DB 2; Length 581;

Best Local Similarity 39.6%; Pred. No. 3.9e-23;

Matches 82; Conservative 27; Mismatches 70; Indels 28; Gaps 7;

QY 1 MARPDPSAPPSTLLLLAQLVGAASAASKAPV-----COEITVPMCRGIGYNTLTHMPN 53

DB 1 MQRPRG-----LMLVLQVMSCAIISMDEPRDQKQPIELPMCDIGYNTMRMN 54

QY 54 QFNHDTODEAGLEVHQFWPLVEIQCSPLDRFLCTMYTPICLPDHHKPLPCRSVCERAK 113

DB 55 LMGHENQREAAIQLHEFAVLEVGCHLRFPLCSLYAPMCTEQVSTPIACRVWCEQAR 114

QY 114 AGCSPLMRQYGFAMPBMSCDRLPYLGRDAEVLCDMD--YNSEATT-----APR 161

DB 115 LKCSPTMEQFNKRPDPSLDCKRLP-NKNDPNYLCMEAPNNSDEPTRSGGLFPPLRFPOR 173

QY 162 PFPKPTLPGPAGAPASGCECPAGGPF 188

DB 174 PHSAGDH-PLKCGGPRGGS-CDNPKGF 198

RESULT 8

S03540

gene frizzled protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Mar-2001

C:Accession: S03540; S15708; S15709

R:Vinson, C.R.; Conover, S.; Adler, P.N. Nature 338, 263-264, 1989

A:Title: A Drosophila tissue polarity locus encodes a protein containing seven potential

A:Reference number: S03540; MUID:89159415; PMID:2493583

A:Accession: S03540

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-581 <VIN>

R:Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L. Genetics 126, 401-416, 1990

A:Title: Molecular structure of frizzled, a Drosophila tissue polarity gene.

A:Reference number: S15708; MUID:91060073; PMID:2174014

A:Accession: S15708

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-581 <AD>

A:Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38460.1; PID:9804979

A:Accession: S15709

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405, 'MY', 408, 'WQFHTIN', <AD2>

A:Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38461.1; PID:9804980

C:Genetics:

A:Gene: FlyBase:fz

A:Cross-references: FlyBase:FBgn0001085

A:Introns: 224/3; 264/3; 329/3; 405/1

C:Superfamily: fruit fly frizzled protein

C:Keywords: alternative splicing; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-581/Product: gene frizzled protein #status predicted <MAT>

Query Match 28.3%; Score 370.5; DB 2; Length 581;

Best Local Similarity 41.1%; Pred. No. 4.7e-22;

Matches 85; Conservative 29; Mismatches 77; Indels 21; Gaps 9;

QY 33 COEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHQFWPLVEIQCSPLDRFLCTMYTP 92

```

      53 CEEITISICKNIPYNTIMNLIGHTKQEBAGLEVHOFADLVKIGCSDDIQLFLCSLYVP
      93 ICPDYHKLPPCRSVCEBAKAGCSPLMRQYGFAMPERMSCDRLPYLGRDAEVLQCMYNN-
      113 VC-TILERPLPPCSLCSARV-CEKLMKTYNFMWPNLECSKFPVAG--GEDLCVAENT
      152 -RSEATTAPRPPRPAPKPTLPGRPPAPASGSGCPAGG-PFYCKCREPVPPI-LKESHPLYN
      169 TSSASTATATRTSAKYAT-----TRKHOTGVESPFRNIGFVC-----PVLKTPLMGMV
      209 KVRTG--QVENCAPVCYQPSFSADERT 223
      218 ELKVGKGLDLDGAPCHAMFFPERERT 244

```

RESULT 9

```

T31690
Hypothetical protein F27E11.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001
C/Accession: T31690
R/Name: P. J. Keppeler, D.
Submitted to the EMBL Data Library, July 1997
A/Description: The sequence of C. elegans cosmid F27E11.
A/Reference number: Z21069
A/Accession: T31690
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-605 <WAM>
A/Cross-references: EMBL:AF016413; PIDN:AA65257.1; GSPDB:GN00023; CESP:F27E11.3
A:Experimental source: strain Bristol N2; clone F27E11
C/Genetics:
A:Gene: CESP:F27E11.3
A:Map position: 5
A:Intons: 28/3; 454/1; 520/1; 562/1
C/Superfamily: fruit fly frizzled protein

```

Query Match

```

      28.0%; Score 366.5; DB 2; Length 605;
      Best local Similarity 37.6%; Pred. No. 1e-21;
      Matches 76; Conservative 25; Mismatches 66; Indels 35; Gaps 5;

```

```

QY 48 LTHMNFNDTODEAGLEVHOFMPLVEIQSPDLRFPLCTMYTPTICLPDYHKLPPCRS
      1 MTFEPNYSYGEKQEBAGLEVHOFPLVEVCFQHLKFLCTMYTPTICQENVDKILPCME
      108 VCBRAKAGCSPLMRQYGFAMPERMSCDRLPYLGRDAEVLQCMYNNRSATAPRPPRPAK
      61 LCVBARKSCSPIMAKYGFMRPETLSICALPKMS-----DOMSTNICAPPDTPKKQ
      168 -----TLGPP- GAPASGSGCPAGG-GPFVCKCREPVPPI-LKESHP
      113 HKGHHKNNQNNQNNHNSYSDGPEVGISKINDVINGBSCQCTCQPFQVASE-----
      207 YNKVRTGQVENCAPVCYQPSFS 228
      169 --KSKVGNVTNCAVSCSPAL 188

```

RESULT 10

```

T25162
Frizzled-1 protein homolog - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Mar-2001
C/Accession: T25162; T42210
R/Name: A.
Submitted to the EMBL Data Library, October 1996
A/Reference number: Z19989
A/Accession: T25162
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-568 <WIL>
A/Cross-references: EMBL:Z81128; PIDN:CAB03398.1; GSPDB:GN00019; CESP:T23D8.1

```

```

A/Experimental source: clone T23D8
R/Schleau, C.E.; Downs, W.D.; Lin, R.; Wiltmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Prie
      Cell 90, 707-716, 1997
A>Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embr
A/Reference number: Z15051; MUID:97433081; PMID:9288750
A/Accession: T42210
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-568 <ROC>
A/Cross-references: EMBL:AF013953; NID:G2463673; PIDN:AAC47750.1; PID:G2463674
C/Genetics:
A:Gene: mom-5; T23D8.1
A:Map position: 1
A:Intons: 158/2; 280/1; 326/2; 407/1; 447/2; 520/2
C/Superfamily: fruit fly frizzled protein

```

Query Match

```

      25.9%; Score 339.5; DB 2; Length 568;
      Best local Similarity 34.0%; Pred. No. 1.3e-19;
      Matches 69; Conservative 35; Mismatches 56; Indels 43; Gaps 7;

```

```

QY 33 COEITVPMCRGIGYNLTTHMNFNDTODEAGLEVHOFMPLVEIQSPDLRFPLCTMYTP
      37 CEHITPMCKNDYNGTVFENLGHITQSEAGPALAQFNPLIKVCSSEDIRLFLCTIVAP
      93 ICPDYHKLPPCRSVCEBAKAGCSPLMRQYGFAMPERMSCDRLPYLGRDAEVLQCMYNN
      97 VCTV-LEKPIQPCRELCLSAKNGCESLMKKFGQWPDQLDCKNFYTD-----LCVGRKS
      153 SEATTAPRPPRPAPKPTLPGRPPAPASGGE-----CP-----AGPFPYCKCREPVPPI
      151 SESSNS-----KSSNDVTFGVSTIANEVVUSPKKCPHMTTSGSH-----SLPL
      200 LKESHPLYNKNVKTGQVENCAPVC 222
      198 L-----SGRLPECSLTC 209

```

RESULT 11

Query Match

```

      25.5%; Score 334; DB 2; Length 197;
      Best local Similarity 35.0%; Pred. No. 1.3e-19;
      Matches 69; Conservative 31; Mismatches 65; Indels 32; Gaps 5;

```

```

QY 15 LLIADLVG-----RAAASKAPVCEITVPMCRGIGYNLTTHMNFNDTODEAGLEVH
      1 MLISIVALLCLWLRLALGVAGPCEAVRIPMCHMPMNITRMNHLHSTQEBVALIAIQ
      70 FPLVLIQSPDLRFPLCTMYTPTICLPDY-HKPLPPCRSVCEBAKAGCSPLMRQYGFAMP
      61 YEELVDVNCSSVSLFPLCMYAPICTLLEPLHDPIKCKSVCCQARDCSEPLMKNYHSMW
      129 ERMSCDRLPYLGR-----DAEVLQCM-----YNNRSEATTAPRPPRPAPPTLPGPGABA
      121 ESLACDELPYDRGVCISSEALVTDLPEDVKMIDITPDMVNGERSDA-----
      178 SGGECPAGGPVYCKCRE 194

```

Query Match

```

      25.5%; Score 334; DB 2; Length 197;
      Best local Similarity 35.0%; Pred. No. 1.3e-19;
      Matches 69; Conservative 31; Mismatches 65; Indels 32; Gaps 5;

```

```

QY 15 LLIADLVG-----RAAASKAPVCEITVPMCRGIGYNLTTHMNFNDTODEAGLEVH
      1 MLISIVALLCLWLRLALGVAGPCEAVRIPMCHMPMNITRMNHLHSTQEBVALIAIQ
      70 FPLVLIQSPDLRFPLCTMYTPTICLPDY-HKPLPPCRSVCEBAKAGCSPLMRQYGFAMP
      61 YEELVDVNCSSVSLFPLCMYAPICTLLEPLHDPIKCKSVCCQARDCSEPLMKNYHSMW
      129 ERMSCDRLPYLGR-----DAEVLQCM-----YNNRSEATTAPRPPRPAPPTLPGPGABA
      121 ESLACDELPYDRGVCISSEALVTDLPEDVKMIDITPDMVNGERSDA-----
      178 SGGECPAGGPVYCKCRE 194

```

Db 169 ---DCKHLSRDRCKCK 182

RESULT 12

frizzled protein 4 - human

C:Species: Homo sapiens (man)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001

C:Accession: J07127

R:Kirkkoti, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 264, 955-961, 1999

A:Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-

A:Reference number: J07127; MUID:20012777; PMID:10544037

A:Accession: J07127

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-537 <KIR>

A:Cross-references: GB:AB032417; DDBJ:AB032417; NID:96277265; PID:96277266

C:Gene(s):

A:Gene: FZD4

A:Map position: 11 region q14 - q21

C:Superfamily: fruit fly frizzled protein

Query Match

Best Local Similarity 23.5%; Score 308; DB 2; Length 537;
Matches 64; Conservative 33; Mismatches 71; Indels 20; Gaps 5;

QY 6 PSAPRL-----LLLLLAQV--RAAASKAVCOEITVPMCRGIVNTHMPNQFNHD 58

Db 11 PGAPGGVGLSLGLLQLLLPARGFGDEERRCPDIRISMCONIGYNTKPNLVGHE 70

QY 59 TODEAGLEVHGFVLEIQCSPDLRFELCTMYTPICLPDVHKPLPCRSVCERAKKAGCSF 118

Db 71 LQTDALQLQTLTFPLIYQCGSSQLQFLCSVYPMCTEKINITIGCGMCLSVKRCER 130

QY 119 LMRQYFANPERNSCDRLPYLGRDAEVLCHDVNRSEATTAAPPPPAKPTLPGRPAAPS 178

Db 131 VKKEFFANPESINCSKFP--QNDHNMCMEGSGDEVPRLPHKT--PIQP----- 177

QY 179 GGECPAGG 186

Db 178 GGECHSVG 185

RESULT 13

J07312

frizzled-3 protein - human

C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001

C:Accession: J07312

R:Salz, C.F.; Forment, E.; Terstappen, G.C.; Caricasole, A.

Biochem. Biophys. Res. Commun. 273, 27-34, 2000

A:Title: Identification, gene structure, and expression of human frizzled-3 (FZD3).

A:Reference number: J07312

A:Accession: J07312

A:Molecule type: mRNA

A:Residues: 1-666 <SAL>

A:Cross-references: GB:A127242

A:Experimental source: brain

C:Comment: This protein, a seven-transmembrane receptor belonging to the frizzled family

possit101 levels in cells.

C:Gene(s):

A:Gene: fzds

A:Map position: 8p21

C:Superfamily: fruit fly frizzled protein

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 22.7%; Score 297; DB 2; Length 666;
Matches 75; Conservative 23; Mismatches 69; Indels 44; Gaps 9;

QY 33 COEITVPMCRGIVNTHMPNQFNHDTODEAGLEVHGFVLEIQCSPDLRFELCTMYTP 92

Db 28 CEPITLRMCQDLPYNTTFEPNLNHYDQTAALANEPFPMVNLCSRFPLCALYAP 87

QY 93 ICLPDVHKPLPCRSVCERAKKAGCSPLMRQYGFANPERNSCDRLPYLGRDAEVLCHDVNR 152

Db 88 ICM-EYGRVTLFCRRLCQAYSECSKLMEMFVPMPEDEKCRFP-----DCD----- 134

QY 153 SBATTAPPPPAKPTLPGR--GAPAS-----GGECPAGGPFVCKRBPVPLKESHIP 205

Db 135 -----EPYRRLVDNLINLAGEPREGAPVAVQRDYGFMC-----RE-----LKIDPD 174

QY 206 L-YMKRTQVPCAVPCYQSPFSADERTFA 235

Db 175 LGYSFL---HVDCSPPCPNMYFRRELSFA 202

RESULT 14

J0164

frizzled-6 protein precursor - human

C:Species: Homo sapiens (man)
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 02-Mar-2001

C:Accession: J0164

R:Tokuhara, M.; Hirai, M.; Atomi, Y.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 243, 622-627, 1998

A:Title: Molecular cloning of human frizzled-6.

A:Reference number: J0164; MUID:98153814; PMID:9480858

A:Accession: J0164

A:Molecule type: mRNA

A:Residues: 1-706 <TOK>

A:Cross-references: GB:AB012911; NID:93062802; PID:NBA25686.1; PID:93062803

C:Comment: This protein is receptor for selected glycoproteins in development and carcin

C:Gene(s):

A:Gene: Hfz6

A:Map position: 8q22.3-q23.1

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:201-222/Domain: transmembrane #status predicted <TM1>

F:233-255/Domain: transmembrane #status predicted <TM2>

F:281-312/Domain: transmembrane #status predicted <TM3>

F:324-345/Domain: transmembrane #status predicted <TM4>

F:370-393/Domain: transmembrane #status predicted <TM5>

F:417-436/Domain: transmembrane #status predicted <TM6>

F:473-495/Domain: transmembrane #status predicted <TM7>

F:38,352/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 21.5%; Score 282; DB 2; Length 706;
Matches 65; Conservative 22; Mismatches 80; Indels 44; Gaps 6;

QY 33 COEITVPMCRGIVNTHMPNQFNHDTODEAGLEVHGFVLEIQCSPDLRFELCTMYTP 92

Db 24 CEPITVPMCRGIVNTHMPNQFNHDTODEAGLEVHGFVLEIQCSPDLRFELCTMYTP 83

QY 93 ICLPDVHKPLPCRSVCERAKKAGCSPLMRQYGFANPERNSCDRLPYLGRDAEVLCHDVNR 152

Db 84 TCIEQIH-VVPCORLCEKVSDDCKLIDTFIGRMBELECRLQYCDRTVPY----- 135

QY 153 SBATTAPPPPAKPTLPGR--GAPAS-----GGECPAGGPFVCKRBPVPLKESHIP 210

Db 136 ---TDPHTFEGFPOKT-----EQVORDIGFWC-----PRHLKT 167

QY 211 RTGQ-----VNCAPVCPQSPFSADERTFA 235

Db 168 SGGQGYKFLIGIOCAPPCPNMYFKSDELEFA 198

RESULT 15

J0174

frizzled protein-2 - human

C:Species: Homo sapiens (man)
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: J0174

R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
 Biochem. Biophys. Res. Commun. 247, 287-293, 1998
 A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
 A:Reference number: JE0174; MID:98308108; PMID:9642118

A:Accession: JE0174

A:Molecule type: mRNA

A:Residues: 1-295 <HUA>

C:Genetics:

A:Map position: 4q

Query Match 20.6%; Score 270.5; DB 2; Length 295;

Best Local Similarity 36.3%; Pred. No. 2.2e-14;

Matches 62; Conservative 26; Mismatches 60; Indels 23; Gaps 7;

```

QY 9 PPSILLILLLAQ-----LVGRAAAASKAPVCOEI--TVPMCRGIGYNLTHMPNOF 55
Db 5 PPSILLILLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIRANLQLCHGIEYQNNRLPNLL 64
QY 56 NMDTQDEAGLEVHQFW-PLVEIQSPDLRPFELCTMYTPICLPDYHKPLPCRSVCERAKA 114
Db 65 GHETMKEV-LEQAGAWIPLVWKQCHPDTKKFLCSLFAVCLDDDETITQCHSLCVQVKD 123
QY 115 GCSPLMQYGFAMPBERMSCDRLPVLGRDAEVLCDYNRSE----ATAPR 161
Db 124 RCAFVMSAFGFWPMDLCCDRFP--ODND-LCIPILASDHLPLPATEAPK 170

```

Search completed: May 19, 2003, 16:34:58

Job time : 24 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:32:11 ; Search time 13 Seconds
(without alignments)
749.764 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPDSPAPSLLLLLAQL.....PNCAPVCYQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	585	1	FZD5_HUMAN
2	1143	87.3	577	1	FZD5_MOUSE
3	825.5	63.0	559	1	FZD5_XENLA
4	824	62.9	694	1	FZD8_HUMAN
5	823.5	62.9	685	1	FZD8_MOUSE
6	802	61.2	581	1	FZD8_XENLA
7	621	47.4	694	1	FRZ2_DROME
8	477	36.4	565	1	FZD2_HUMAN
9	476	36.3	570	1	FZD2_MOUSE
10	466	35.6	574	1	FZD2_RAT
11	457	34.9	574	1	FZD7_HUMAN
12	440.5	33.6	572	1	FZD7_MOUSE
13	438.5	33.5	551	1	FZD2_XENLA
14	431	32.9	592	1	FZD1_CHICK
15	422	32.2	623	1	FZD1_MOUSE
16	421	32.1	523	1	FZD2_CHICK
17	414.5	31.6	648	1	FZD1_HUMAN
18	411	31.4	567	1	FZD7_CHICK
19	405.5	31.0	549	1	FZD7_XENLA
20	401	30.6	559	1	FZD1_XENLA
21	398	30.4	641	1	FZD1_RAT
22	394.5	30.1	591	1	FZD9_HUMAN
23	394.5	30.1	592	1	FZD9_MOUSE
24	384	29.3	581	1	FZ10_HUMAN
25	372	28.4	325	1	FRZB_HUMAN
26	371	28.3	583	1	FRIZ_DROME
27	370.5	28.3	581	1	FRIZ_DROVI
28	368	28.1	586	1	FZD4_XENLA
29	367	28.0	323	1	FRZB_MOUSE
30	366	27.9	325	1	FRZB_BOVIN
31	360	27.5	580	1	FZD8_XENLA
32	351	26.8	585	1	FZD10_CHICK
33	309	23.6	523	1	FZD4_XENLA

ALIGNMENTS

RESULT 1
FZD5_HUMAN STANDARD; PRT; 585 AA.
AC Q13467;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frlzzled 5 precursor (Frlzzled-5) (Fz-5) (Fz5) (Fz5).
GN FZD5 OR HFZ5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96224032; PubMed=8626800;
RA Wang Y., Mcke J.P., Abella B.S., Andreasen K., Worley P.,
RT Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.,
RT "A large family of putative transmembrane receptors homologous to the
RT product of the Drosophila tissue polarity gene frizzled.";
RT J. Biol. Chem. 271:4468-4476(1996).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=21301556; PubMed=11408929;
RA Satoh T., Hirai M., Katoh M.,
RT "Molecular cloning and characterization of human Frlzzled-5 gene on
RT chromosome 2q33.3-q34 region.";
RT Int. J. Oncol. 19:105-110(2001).
RN (3)
RP SEQUENCE OF 273-331 FROM N.A.
RC TISSUE=oesophageal carcinoma;
RX MEDLINE=98374323; PubMed=9707618;
RA Tanaka S., Akiyoshi T., Mori M., Wada J.R., Sugimachi K.,
RT "A novel frizzled gene identified in human esophageal carcinoma
RT mediate APC/beta-catenin signals.";
RT Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
RN (4)
RP COUPLING TO BETA-CATENIN PATHWAY.
RX MEDLINE=9720741; PubMed=9054360;
RA He X., Saint-Jean J.P., Wang Y., Nathans J., David I., Varmus H.,
RT "A member of the Frlzzled protein family mediating axis induction by
RT Wnt-5A.";
RT Science 275:1652-1654(1997).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins, inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated

CC tissues. Interacts specifically with wnt5a to induce the beta-catenin pathway.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (by similarity) (By similarity).

CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC -----

CC EMBL; U43318; AAC50385.1; -

CC EMBL; AB043702; BAB60959.1; -

CC Gene; HGNC:4043; FZD5.

CC MIM; 601723; -

CC DR InterPro; IPR000539; Frizzled.

CC DR InterPro; IPR000024; Fz domain.

CC DR InterPro; IPR000832; GPCR_secretin.

CC DR Pfam; PF01392; Fz; 1.

CC DR Pfam; PF01534; Frizzled; 1.

CC DR PRINTS; PRO0489; FRIZZLED.

CC DR SMART; SM00063; FRI; 1.

CC DR PROSITE; PSS0038; FZ; 1.

CC DR PROSITE; PSS0261; G-PROTEIN RECEPTOR F2; 1.

CC DR Multigene family; G-protein coupled receptor; Transmembrane;

CC KM Developmental protein; Glycoprotein; Signal.

CC FT SIGNAL 1 26

CC FT CHAIN 27 585

CC FT DOMAIN 27 238

CC FT TRANSMEM 239 259

CC FT DOMAIN 260 270

CC FT TRANSMEM 271 291

CC FT DOMAIN 292 315

CC FT TRANSMEM 316 336

CC FT DOMAIN 337 358

CC FT TRANSMEM 359 379

CC FT DOMAIN 380 402

CC FT TRANSMEM 403 423

CC FT DOMAIN 424 449

CC FT TRANSMEM 450 470

CC FT DOMAIN 471 500

CC FT TRANSMEM 501 521

CC FT DOMAIN 522 585

CC FT TRANSMEM 523 530

CC FT SITE 583 585

CC FT CARBOHYD 47 47

CC FT CARBOHYD 151 151

CC FT CONFLICT 88 88

CC FT CONFLICT 262 263

CC FT CONFLICT 345 345

CC FT CONFLICT 357 357

CC FT CONFLICT 402 402

CC FT CONFLICT 402 402

CC SQ SEQUENCE 585 AA; 64551 MW; CF66C5BA746E7971 CRC64;

Query Match 100.0%; Score 1110; DB 1; Length 585;

Best Local Similarity 100.0%; Pred. No. 1.8e-95;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARPDSAPPSLLILLIAQLVGRRAAASKAPVCCOETVPMCRGIGVNLTHMPQFNHDQ 60

DB 1 MARPDSAPPSLLILLIAQLVGRRAAASKAPVCCOETVPMCRGIGVNLTHMPQFNHDQ 60

OY 61 DEAGLEVHGFVPLVEIQCSDDLRFLLCTMTPTPICLPDYHKLPPCRSVCERAKAGCSPLM 120

DB 61 DEAGLEVHGFVPLVEIQCSDDLRFLLCTMTPTPICLPDYHKLPPCRSVCERAKAGCSPLM 120

OY 121 ROYGFAMPWRMSCDRLPVGLDAEVLQMDYNSSEATTAPRPFPAPKTLPGPGAGASG 180

DB 121 ROYGFAMPWRMSCDRLPVGLDAEVLQMDYNSSEATTAPRPFPAPKTLPGPGAGASG 180

OY 181 ECPAGGPFVCKCEPFPVPLIKESHPIYNKVRIGQVNCVPCYQSPFSADERTFA 235

DB 181 ECPAGGPFVCKCEPFPVPLIKESHPIYNKVRIGQVNCVPCYQSPFSADERTFA 235

RESULT 2

FZD5_MOUSE STANDARD; PRT; 577 AA.

ID FZD5_MOUSE

AC Q9E0D0; O08975;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (mFz5).

GN FZD5.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6N; TISSUE=Gut;

RX PubMed=11092808;

RA Ishikawa T., Tamai Y., Zorn A.M., Yoshida H., Seldin M.F.,

RA Nishikawa S.-I., Takeo M.M.;

RT "Mouse Wnt receptor gene Fzd5 is essential for yolk sac and placental angiogenesis.";

RL Development 128:25-33(2001).

RN [2]

RP SEQUENCE OF 207-286 FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Prostate;

RA Johnson M.A., Greenberg N.M.;

RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.

RN [3]

RP TISSUE SPECIFICITY.

RX MEDLINE=96224032; PubMed=8626800;

RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,

RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;

RT "A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled.";

RL J. Biol. Chem. 271:4468-4476(1996).

CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Plays a role in yolk sac angiogenesis and in placental vascularization. Binds to Wnt2, Wnt10B, Wnt5A, but not to Wnt2B or Wnt4.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes, epithelial cells of the small intestine and goblet cells of the colon.

CC -1- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also expressed in the placental blood vessel of embryonic origin.

CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: AF272146; AAC39355.1; -
 CC EMBL: AF005203; AAC01953.1; -
 CC MGI: 108571; Fz5.
 CC InterPro: IPR000539; Frizzled.
 CC InterPro: IPR000024; Fz_domain.
 CC InterPro: IPR000832; GPCR_secretin.
 CC Pfam: PF01392; Fz; 1.
 CC Pfam: PF01534; Frizzled; 2.
 CC PRINTS: PR00489; FRIZZLED.
 CC SMART: SM00063; FRI; 1.
 CC PROSITE: PS50038; Fz; 1.
 CC PROSITE: PS50261; G-PROTEIN RECEPTOR Fz; 4; 1.
 CC Multigene family; G-protein coupled receptor; Transmembrane;
 CC Developmental protein; Glycoprotein; Signal.
 CC SIGNAL 1 26
 CC CHAIN 1 27 577
 CC DOMAIN 27 234
 CC TRANSMEM 235 255
 CC DOMAIN 256 266
 CC TRANSMEM 267 287
 CC DOMAIN 288 311
 CC TRANSMEM 312 332
 CC DOMAIN 333 354
 CC TRANSMEM 355 375
 CC DOMAIN 376 398
 CC TRANSMEM 399 419
 CC DOMAIN 420 445
 CC TRANSMEM 446 466
 CC DOMAIN 467 495
 CC TRANSMEM 496 516
 CC DOMAIN 517 577
 CC TRANSMEM 578 598
 CC SITE 575 577
 CC CARBOHYD 47 47
 CC CARBOHYD 151 151
 CC SEQUENCE 577 AA; 63794 MW; F6877C9B535C865 CRC64;

Query Match 87.3%; Score 1143; DB 1; Length 577;
 Best Local Similarity 91.1%; Pred. No. 2e-82;
 Matches 214; Conservative 3; Mismatches 14; Indels 4; Gaps 3;

QY 1 MARPPSAPPSSLLLLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNLTTHMPQFNHDTQ 60
 DB 1 MARPPSAPPSSLLLLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNLTTHMPQFNHDTQ 60
 QY 61 DEAGLEVHOFWPLVBIQCSBDLRFICTMYTPICLPDYHKPLPCSSVCERAYAGCSPLM 120
 DB 61 DEAGLEVHOFWPLVBIQCSBDLRFICTMYTPICLPDYHKPLPCSSVCERAYAGCSPLM 120
 QY 121 ROYGFAPWRMSCDRLPVYGRDAEVLCMDYNSSEATAPRRPAPRPTLPGRPGAAASGG 180
 DB 121 ROYGFAPWRMSCDRLPVYGRDAEVLCMDYNSSEATAPRRPAPRPTLPGRPGAAASGG 180
 QY 181 ECPAGGPFVCKREPFVPLIKESHPLYNKYRTGOVPCNCAVPCQPSFSADERTFA 235
 DB 181 ECPAGGPFVCKREPFVPLIKESHPLYNKYRTGOVPCNCAVPCQPSFSADERTFA 235
 DB 180 ECGHRRVQS--EPFVPLIKESHPLYNKYRTGOVPCNCAVPCQPSFSADERTFA 231

RESULT 3
 FZD5_XENLA STANDARD: PRT: 559 AA.
 AC P58421;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)

DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (Xfz5).
 GN FZ5.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OK NCBI_TaxID=8335;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21233029; PubMed=11335120;
 RA Sumnas S., Ekker S.C.,
 RT "Xenopus frizzled-5: a frizzled family member expressed exclusively in
 RL the neural retina of the developing eye.";
 Mech. Dev. 103:133-136(2001).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in retina.
 CC -1- DEVELOPMENTAL STAGE: First detected at the late neurula stage in
 CC retinal primordia. Throughout the tailbud stage, expressed
 CC exclusively in the neural retina within the optic vesicles. During
 CC tadpole stage, expression becomes restricted to the ciliary
 CC marginal zone.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Trip motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTRAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: AF300716; AAK51688.1; -
 CC InterPro: IPR000539; Frizzled.
 CC InterPro: IPR000024; Fz_domain.
 CC InterPro: IPR000832; GPCR_secretin.
 CC Pfam: PF01392; Fz; 1.
 CC Pfam: PF01534; Frizzled; 1.
 CC PRINTS: PR00489; FRIZZLED.
 CC SMART: SM00063; FRI; 1.
 CC PROSITE: PS50038; Fz; 1.
 CC PROSITE: PS50261; G-PROTEIN RECEPTOR Fz; 4; 1.
 CC Multigene family; G-protein coupled receptor; Transmembrane;
 CC Developmental protein; Glycoprotein; Signal.
 CC SIGNAL 1 26
 CC CHAIN 1 27 559
 CC DOMAIN 27 220
 CC TRANSMEM 221 241
 CC DOMAIN 242 257
 CC TRANSMEM 258 278
 CC DOMAIN 279 301
 CC TRANSMEM 302 322
 CC DOMAIN 323 343
 CC TRANSMEM 344 364

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FT DOMAIN 365 387 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 388 408 5 (POTENTIAL)
FT DOMAIN 409 434 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 435 455 6 (POTENTIAL)
FT DOMAIN 456 483 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 484 504 7 (POTENTIAL)
FT DOMAIN 505 559 CYTOPLASMIC (POTENTIAL)
FT DOMAIN 28 149 FZ.
FT DOMAIN 152 157 LYS-THR-X-X-TRP MOTIF.
FT SITE 507 512 PDZ-BINDING.
FT SITE 557 559 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 559 AA; 63518 MW; 581EB243FCB954B7 CRC64;

Query Match 63.0%; Score 825.5; DB 1; Length 559;
Best Local Similarity 69.2%; Pred. No. 1.3e-57;
Matches 153; Conservative 20; Mismatches 35; Indels 13; Gaps 4;

QY 14 LLLLAQLVGRRAAASKAPVCEITVPMCRGIGYVLTMPNPFNDTQDEAGLEVHGFVPL 73
DB 14 VLLLDYFAFAQAASKAIVCEITVPMCRGIGYVLTMPNPFNDTQDEAGLEVHGFVPL 73
QY 74 VETQSPDLRFCTMTPTICLPDYHKLPPCSVCERANAGCSPLMRYGFAMPERMSC 133
DB 74 VVIQCSLDLKFPLCSMTPTICLPDYHKLPPCSVCERANAGCSPLMRYGFAMPERMSC 133
QY 134 DRIPVLRGDAVCMQVNRSEATAPRPPAPKPTLPPGAPASGEGCAGGPFVCKR 133
DB 134 DRIPERHG-DDPTLCMYNMTETTTTP-----PTHPPKVKVTPS--DCDG---VCKCR 180
QY 194 EPEVPIKESHPLYNKRVQGVNCAVPCYQSPFSADERT 234
DB 181 EPEVITRESHPLYNKRVQGVNCAVPCYQSPFSADERT 221

RESULT 4
FZD8 HUMAN STANDARD; PRT; 694 AA.
ID FZD8 HUMAN
AC 09H461;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (hFz8).
GN FZD8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RX SEQUENCE FROM N.A.
RX MEDLINE=21192958; PubMed=11295046;
RA Saitoh T., Hirai M., Katoh M.;
RT "Molecular cloning and characterization of human Frizzled-8 gene on
RT chromosome 10p11.2."
RL Int. J. Oncol. 18:991-996 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins. Inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated

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CC tissues.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Most abundant in fetal kidney, followed by
CC brain and lung. In adult tissues, expressed in kidney, heart,
CC pancreas and skeletal muscle.
CC -1- DOMAIN: Lys-thr-X-X-X-Tip motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
CC DR EMBL; AB043703; BAB41064.1; -
CC DR EMBL; AL121749; CAC10185.1; -
CC DR Genew; HGNC:4046; FZD8.
CC DR MIM; 606146; -
CC DR InterPro; IPR000539; Frizzled.
CC DR InterPro; IPR000024; Fz domain.
CC DR InterPro; IPR000832; GPCR_secretin.
CC DR Pfam; PF01392; Fz; 1.
CC DR Pfam; PF01534; Frizzled; 1.
CC DR PRINTS; PR00489; FRIZZLED.
CC DR SMART; SM00063; FRI; 1.
CC DR PROSITE; PS50038; Fz; 1.
CC DR PROSITE; PS50038; Fz; 1.
CC DR Multigene family; G-protein-coupled receptor; Transmembrane;
CC KW Developmental protein; Glycoprotein; Signal.
CC FT SIGNAL 1 27
CC FT CHAIN 28 694
CC FT DOMAIN 28 275 FRIZZLED 8.
CC FT TRANSMEM 276 296 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 297 312 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 313 333 2 (POTENTIAL).
CC FT DOMAIN 334 396 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 397 417 3 (POTENTIAL).
CC FT DOMAIN 418 439 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 440 460 4 (POTENTIAL).
CC FT DOMAIN 461 483 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 484 504 5 (POTENTIAL).
CC FT DOMAIN 505 532 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 533 553 6 (POTENTIAL).
CC FT DOMAIN 554 584 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 585 604 7 (POTENTIAL).
CC FT DOMAIN 606 694 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 30 151 FZ.
CC FT DOMAIN 168 172 POLY-PRO.
CC FT DOMAIN 194 202 POLY-GLY.
CC FT DOMAIN 211 216 POLY-GLY.
CC FT DOMAIN 639 663 POLY-GLY.
CC FT SITE 608 613 LYS-THR-X-X-TRP MOTIF.
CC FT SITE 692 694 PDZ-BINDING.
CC FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 694 AA; 73300 MW; E740CBFDDA2A233EF CRC64;

Query Match 62.9%; Score 824; DB 1; Length 694;
Best Local Similarity 59.9%; Pred. No. 2.1e-57;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 LLLLAQLVGRRAAASKAPVCEITVPMCRGIGYVLTMPNPFNDTQDEAGLEVH 68
DB 11 LLLLAQLVGRRAAASKAPVCEITVPMCRGIGYVLTMPNPFNDTQDEAGLEVH 70

```

QY 69 QFWPLVEICSPDLRFLLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQGFAMP 128
 DB 71 QFWPLVEICSPDLRFLLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQGFAMP 130
 QY 129 ERMSCDRLPVLGRDAVLCMDYNRSEATTA---PPRPPAKFTLPG-----PPG 174
 DB 131 DMRKCDRLPEQG-NPDTLCMDYNRKTDLTAAAPPRRLPPP--PGEOPSSGSHRPPG 187
 QY 175 A-----PASGG-----ECPAGGPFV---CKREPFVPLKESH 205
 DB 188 ARPPHRRGGSGGGGDAAPAPRAGGGGGGKARPPGGAAACPCGCCCRAMVSVSSERHP 247
 QY 206 LYNKRTGVPCNCAVPCYOPSSADERTF 234
 DB 248 LYNKRTGVPCNCAVPCYOPSSADERTF 276

RESULT 5
 FZD8_MOUSE STANDARD; PRT; 685 AA.
 ID FZD8_MOUSE 061091;
 AC 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (MF28).
 GN FZD8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96224032; PubMed=8626800;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Morley P.,
 RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.,
 RA "A large family of putative transmembrane receptors homologous to the
 product of the Drosophila tissue polarity gene frizzled.";
 RT J. Biol. Chem. 271:4468-4476 (1996).
 RL (2)
 RP COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=99324245; PubMed=10395542;
 RA Sheidahl L.C., Park M., Malbon C.C., Moon R.T.,
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 homologs in a G-protein-dependent manner.";
 RL Curr. Biol. 9:695-698 (1999).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins, inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. Activation by Wnt8 induces expression of beta-catenin
 target genes.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in chondrocytes.
 CC -1- DOMAIN: Lys-Thr-X-X-Tyr motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U43321; AAC52433.1; -
 DR MGD; MGI:108460; Fzdb.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G-PROTEIN RECP F2 4; 1.
 DR Multigene family; G-protein coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 27
 FT CHAIN 1 685
 FT DOMAIN 28 272
 FT TRANSMEM 273 293
 FT DOMAIN 294 309
 FT TRANSMEM 310 330
 FT DOMAIN 331 394
 FT TRANSMEM 395 415
 FT DOMAIN 416 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 481
 FT TRANSMEM 482 502
 FT DOMAIN 503 530
 FT TRANSMEM 531 551
 FT DOMAIN 552 582
 FT TRANSMEM 583 603
 FT DOMAIN 604 685
 FT DOMAIN 30 151
 FT DOMAIN 168 173
 FT DOMAIN 353 361
 FT DOMAIN 640 654
 FT SITE 606 611
 FT SITE 683 685
 FT CARBOHYD 49 49
 FT CARBOHYD 152 152
 FT CARBOHYD 473 473
 SQ SEQUENCE 685 AA; 73215 MW; F333B49474411267 CRC64;
 Query Match 62.9%; Score 823.5; DB 1; Length 685;
 Best Local Similarity 60.0%; Pred. No. 236-57;
 Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
 QY 11 SLL--LTLIAQLVGRRAAASAKAPVCOEIVPMCRGIGYVLTMPNQFNHDTODEAGLEVH 68
 DB 11 SLLAALAVIGRRSGAAASAKELACOEIVPLCKIGVYTTMPNQFNHDTODEAGLEVH 70
 QY 69 QFWPLVEICSPDLRFLLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQGFAMP 128
 DB 71 QFWPLVEICSPDLRFLLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQGFAMP 130
 QY 129 ERMSCDRLPVLGRDAVLCMDYNRSEATTA---PPRPPAKFTLPG-----PPG 174
 DB 131 DMRKCDRLPEQG-NPDTLCMDYNRKTDLTAAAPPRRLPPP--PGEOPSSGSHRPPG 188
 QY 175 A-----PASGG-----ECPAGGPFV---CKREPFVPLKESH 209
 DB 188 ARPPHRRGGSGGGGDAAPAPRAGGGGGGKARPPGGAAACPCGCCCRAMVSVSSERHP 248
 QY 210 VRTGVPCNCAVPCYOPSSADERTF 234
 DB 249 VRTGVPCNCAVPCYOPSSADERTF 273

RESULT 6
 FZD8_XENLA STANDARD; PRT; 581 AA.
 ID FZD8_XENLA

AC 093274; Q9Y155;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (Xfz8).
 GN FZ8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OK NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RC TISSUE=embryo;
 RX PubMed=9651509;
 RA Itoh K., Jacob J., Sokol S.Y.;
 RT "A role for Xenopus Frizzled 8 in dorsal development.";
 RL Mech. Dev. 74:145-157(1998).
 (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=98301424; PubMed=9636083;
 RA Deardorff M.A., Tan C., Conrad L.J., Klein P.S.;
 RT "Frizzled-8 is expressed in the Spemann organizer and plays a role in
 early morphogenesis.";
 RL Development 125:2687-2700(1998).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins, inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. Activation by Wnt8, Wnt5A or Wnt3A induces expression of
 beta-catenin target genes. Displays an axis-inducing activity.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: First expressed at high levels in the late
 blastula stages. At early gastrula, expressed in the deep cells of
 the Spemann organizer prior to involution of the dorsal blastopore
 lip. Detected in presumptive neuroectoderm as gastrulation
 proceeds. Becomes restricted to the anterior ectoderm by the end
 of gastrulation. At neurula stages, localized in the most anterior
 region of the embryo, mainly in the anterior ectoderm including
 telencephalic and cement gland regions.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (by similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (by
 similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL, AF011777, AAC31121.1, -;
 DR EMBL, AF033110, AAC7361.1, -;
 DR InterPro, IPR000539, Frizzled.
 DR InterPro, IPR000024, Fz domain.
 DR InterPro, IPR000832, GPCR_secretin.
 DR Pfam, PF01392, Fz; 2.
 DR Pfam, PF01534, Frizzled; 2.
 DR PRINTS, PR00489, FRIZZLED.

DR SMART, SM00063; FRI, 1.
 DR PROSITE, PS50038; FZ, 1.
 DR PROSITE, PS50261; G-PROTEIN RECEPTOR F2.4; 1.
 KW Multigene family: G-protein coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 24
 FT DOMAIN 24 581
 FT DOMAIN 24 239
 FT TRANSMEM 240 260
 FT DOMAIN 261 271
 FT TRANSMEM 272 292
 FT DOMAIN 293 320
 FT TRANSMEM 321 341
 FT DOMAIN 342 377
 FT TRANSMEM 378 398
 FT DOMAIN 399 407
 FT TRANSMEM 408 428
 FT DOMAIN 429 454
 FT TRANSMEM 455 475
 FT DOMAIN 476 505
 FT TRANSMEM 506 526
 FT DOMAIN 527 581
 FT SITE 24 144
 FT SITE 529 534
 FT SITE 579 581
 FT CARBOHYD 42 42
 FT CARBOHYD 146 146
 FT CONFLICT 1 3
 FT CONFLICT 7 7
 FT CONFLICT 10 10
 FT CONFLICT 14 14
 FT CONFLICT 20 20
 FT CONFLICT 135 135
 FT CONFLICT 171 171
 FT CONFLICT 175 175
 FT CONFLICT 185 185
 FT CONFLICT 216 216
 FT CONFLICT 237 237
 FT CONFLICT 494 496
 FT CONFLICT 500 500
 FT CONFLICT 547 547
 FT CONFLICT 565 565
 FT CONFLICT 572 572
 SQ SEQUENCE 581 AA; 65378 MW; 80890C408AB21E23 CRC64;
 Query Match 61.2%; Score 802; DB 1; Length 581;
 Best Local Similarity 63.9%; Pred. No. 9.5e-56;
 Matches 149; Conservative 25; Mismatches 43; Indels 16; Gaps 5;
 QY 13 LLLLLAQLVGRRAAASAKAVCOEITVPMCRGIGYNLTNPNQFNHDTODAGLEVHQFMP 72
 DB 8 LLLVSWLWGSGCAAKKELSCOEITVPLCKDIGYNTVMPNQNHDTOEAGNEVHQFMP 67
 QY 73 LVETQSPDLRFFLCTMTYPTICPDYHKPLPCRSYCEBAKACGSLPMQYGFAMEERMS 132
 DB 68 LVVTHCSPLKFKPLCSMTYPTICLEDYKKPLPCRSYCEBARACAPLMQYGFAMPDRMR 127
 QY 133 CDRPLVIGDAEVLCDMD-VNRSEATT-APPRPAPAV-----TLGPPGAPASGGE 181
 DB 128 CDRPLVIGDAEVLCDMD-VNRSEATT-APPRPAPAV-----TLGPPGAPASGGE 186
 QY 182 CPAGSPFVCKREPFVILKESHPLYNKYRTQVPCAVCYQSPFSADERT 234
 DB 187 CEGS-----CGCRAPMVQVSNERNRPLVNRVTRTQIPRCAPCHNPFSPBERRTP 235
 RESULT 7
 FRZ2 DROME STANDARD; PRT; 694 AA.
 ID FRZ2 DROME
 AC 094916;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled protein 2 precursor (Frizzled-2) (DFZ2).
 GN F22 OR CG9739.
 OC Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=1221;
 RN (1)
 RP SEQUENCE FROM N.A., AND BINDING TO WINGLESS THROUGH FZ DOMAIN.
 RX MEDLINE=69353971; PubMed=8717036;
 RA Bhatot P., Brink M., Samos C.H., Hsieh J.C., Wang Y., Macke J.P.,
 RA Andrew D., Nathans J., Nusse R.,
 RT "A new member of the frizzled family from Drosophila functions as a
 RT wingless receptor.";
 RL Nature 382:225-230(1996).
 (12)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt A., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bence P.V., Bernick B.P., Bhandari D., Bolshakov S.,
 RA Borovoy D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Maassman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins. Inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. Required to coordinate
 CC the cytoskeletons of epidermal cells to produce a parallel array
 CC of cuticular hairs and bristles.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- DEVELOPMENTAL STAGE: Expression starts at stage 6 in all cells
 CC between 15 and 70 per cent of egg length, including the
 CC invaginating cells of the ventral furrow. Stripe pattern is

emerging by early stage 8. From stage 9 and continuing throughout
 embryogenesis, expression is seen in the developing CNS. At stage
 10, expressed in 15 stripes in the presumptive head and trunk
 regions, in the posterior midgut primordium, in a subset of cells
 of anterior midgut invagination and in the procephalic lobe. At
 stage 12, expression declines in epidermis and increases in the
 midgut and visceral mesoderm. At stage 17, only expressed in the
 CNS, hindgut and dorsal vessel.
 CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands.
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SWO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC -----

DR EMBL; U65589; AAC47273.1; -
 DR EMBL; AE003518; AAF49184.1; -
 DR FlyBase; FBgn0016797; fz2.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR_reccetin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS00318; FZ; 1.
 DR PROSITE; PS50261; G-PROTEIN_RECEP_F2_4; 1.
 DR KEGG; MultiGene family; Receptor; G-protein coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL. 1 22
 FT CHAIN. 23 694
 FT DOMAIN. 23 315
 FT TRANSMEM. 316 336
 FT DOMAIN. 337 352
 FT TRANSMEM. 353 373
 FT DOMAIN. 374 397
 FT TRANSMEM. 398 418
 FT DOMAIN. 419 439
 FT TRANSMEM. 440 460
 FT DOMAIN. 461 482
 FT TRANSMEM. 483 503
 FT DOMAIN. 504 534
 FT TRANSMEM. 535 555
 FT DOMAIN. 556 584
 FT TRANSMEM. 585 605
 FT DOMAIN. 606 694
 FT DOMAIN. 187 225
 FT DOMAIN. 59 180
 FT SITE. 608 613
 FT SITE. 682 694
 FT CARBOHYD. 78 78
 FT CARBOHYD. 288 288
 FT CONFLICT. 55 55
 FT CONFLICT. 417 417
 SO SEQUENCE. 694 AA; 75451 MW; 6C310F13CAFP096 CRC64;

Query Match 47.4%; Score 621; DB 1; Length 694;
 Best Local Similarity 43.4%; Pred. No. 1.6e-41;
 Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY 22 GRAAASKRP-----VCOEIVPMCGRGVNLTHMPNPFNHDODAGLEVH 68
 DB 40 GAGLDASPAAGVGVPIPDNLRCEITTPMCRGIGVNMSTNHEHODAGLEVH 99
 QY 69 QFWPLVEIOCSPLRPFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLMRQYFAMP 128


```

Db 100 QFWPLVEIKSPDLKFLKCMYTPICLEDYHKPLPVCRCVSCERARSGCAPIMOOYSEMP 159
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 129 ERMSCDRLPVLGDAEVLCDMDY----- 150
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 160 ERVACEHLPLHG-DPDLVLCMEQPSYTEAGSGSGSGSGSGSGSGGCKRKGSGSGGS 218
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 151 ----NNSSEATAPRPFPAPPTLPGPGAPASGEGCPAGGPFVCKREPFV----- 197
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 219 GAGSGSGSTTKPCRGNSK-NCNPGGKASGREGS-----CSCRSPLIFLGKQLQ 271
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 198 ----PLIKESHPLYNKV---RTGQVNCVPCYQSPFSADERTFA 235
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 272 QQSQMPMHHPHWMYMLTVQRIAGVNCGIPCKGPFPSNDEKQFA 317
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
FZD2_HUMAN STANDARD; PRT; 565 AA.
ID FZD2_HUMAN
AC Q14332;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 2 precursor (Frizzled-2) (Fz-2) (Fz2) (FZE2)
GN FZD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA MEDLINE=96044450; PubMed=7558010;
RT Zhao Z., Lee C.C., Baldini A., Caskey C.T.;
RT "A human homologue of the Drosophila polarity gene frizzled has been
RT identified and mapped to 17q21.1.";
RL Genomics 27:370-373(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RA MEDLINE=99032814; PubMed=9813155;
RT Sagara N., Toda G., Hirai M., Terada M., Katoh M.;
RT "Molecular cloning, differential expression, and chromosomal
RT localization of human frizzled-1, frizzled-2, and frizzled-7.";
RL Biochem. Biophys. Res. Commun. 252:117-122(1998).
RN [3]
RP SEQUENCE OF 282-343 FROM N.A.
RC TISSUE=Oesophageal carcinoma;
RA MEDLINE=98374323; PubMed=9707618;
RT Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.;
RT "A novel frizzled gene identified in human esophageal carcinoma
RT mediates APC/beta-catenin signals.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins, inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated
CC tissues.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed. In the adult, mainly found
CC in heart, placenta, skeletal muscle, lung, kidney, pancreas,
CC prostate, testis, ovary and colon. In the fetus, expressed in
CC brain, lung and kidney. Low levels in fetal liver.
CC -1- DOMAIN: Lys-Thr-X-X-Tip motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).

```

```

CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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CC -----
CC EMBL: L37882; AAB46397.1; -.
CC EMBL: AB017364; BAA34667.1; -.
CC Genew; HGNC:4040; FZD2.
CC MIM; 600667; -.
CC DR InterPro; IPR000539; Frizzled.
CC DR InterPro; IPR000024; Fz domain.
CC DR InterPro; IPR000832; GPCR_secretin.
CC DR Pfam; PF01392; Fz; 1.
CC DR Pfam; PF01534; Frizzled; 1.
CC DR SMART; SM00489; FRIZZLED.
CC DR SMART; SM00063; FRI; 1.
CC DR PROSITE; PS50261; G-PROTEIN RECEPTOR_FZ_4; 1.
CC DR PROSITE; PS50261; G-PROTEIN RECEPTOR_FZ_1.
CC KW Multigene family; G-protein coupled receptor; Transmembrane;
CC Developmental protein; Glycoprotein; Signal.
CC -----
CC FT SIGNAL 1 23
CC FT CHAIN 1 23
CC FT DOMAIN 24 565
CC FT DOMAIN 24 247
CC FT TRANSMEM 248 268
CC FT DOMAIN 269 279
CC FT TRANSMEM 280 300
CC FT DOMAIN 301 327
CC FT TRANSMEM 328 348
CC FT DOMAIN 349 370
CC FT TRANSMEM 371 391
CC FT DOMAIN 392 414
CC FT TRANSMEM 415 435
CC FT DOMAIN 436 461
CC FT TRANSMEM 462 482
CC FT DOMAIN 483 519
CC FT TRANSMEM 520 540
CC FT DOMAIN 541 565
CC FT DOMAIN 34 153
CC FT DOMAIN 181 187
CC FT SITE 543 548
CC FT SITE 563 565
CC FT CARBOHYD 53 53
CC FT CARBOHYD 154 154
CC SO SEQUENCE 565 AA; 63554 MW; AAB387876A1DDE063 CR664;

Query Match 36.4%; Score 477; DB 1; Length 565;
Best Local Similarity 41.9%; Pred. No. 2,4e-30;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

Qy 3 RPPSPAPPSLLILLALQVGRRAAASKAPV-----CQETVPMCRGICYNLTTHPNOR 55
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2 RPPSAPRLLPLPLLLPAAAPPAQFHEKGISPDHFCOPISILPTDIAVNOTIMNLL 61
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 56 NHQTOEAGLEVHQPMPVLEIQCSPDLRFPLCTMYTPICLDYHKPLPVCRCVSCERAKAG 115
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 GHTNODGAGLEVHQPMPVLEIQCSPDLRFPLCTMYTPICLDYHKPLPVCRCVSCERAKAG 120
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 116 CSPLMRQYGFAMERMSCDRLPVLGDAEVLCDMDYNSR-----ATAPRPFPFA-KPT 168
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 CELALMKKFGQWERLRCHEFRHNG--AEDICVGHNSHEDGAPALTTAP--PGIOPG 175
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 169 LPPPGAPASGSGCPAGG---PFVCKREPFVPLIKESHPLYNKVRTGQVNCVPCYQ 224
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 176 AGGTPGGPGGGAPPPYATLEHFFHCP-----RVKLV--PSYLSYKFLGERDCAAPC-E 226
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```


Qy 225 PS-----FSADERTFA 235
 Db 227 PARPDGSMFFSQEETRFA 244

RESULT 9
 ID FZD2_MOUSE STANDARD; PRT; 570 AA.
 AC Q9JIF6; Q9JIF5; Q9MU2;
 DT 15-JUN-2002 (Rel. 41, Last created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE FZD2 OR FZD10.
 GN FZD2 OR FZD10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 OK NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Fetal gut;
 RX MEDLINE=20363524; PubMed=10903145;
 RA Malik T.H., Shivdasani R.A.;
 RT "Structure and expression of a novel frizzled gene isolated from the
 RT developing mouse gut.";
 RT Biochem. J. 349:829-834(2000).
 RL (2)
 RP SEQUENCE OF 172-312 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Prostate;
 RA Johnson M.A., Greenberg N.M.;
 RT "Characterization of the wnt signaling cascade in the TRAMP transgenic
 RT mouse model of prostate cancer.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in embryonic and adult heart, lung,
 CC chondrocytes and brain. Also expressed in the developing
 CC gastrointestinal tract (strongest in foregut), much weaker
 CC expression in the adult. No expression in fetal liver and adult
 CC spleen. Up-regulated in oesophageal squamous cell carcinomas.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC
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 CC
 CC EMBL; AF206321; AAF74056.1; -
 CC EMBL; AF206322; AAF74057.1; -
 CC EMBL; AF139183; AAD28286.1; -
 CC MGD; MG1:1888513; Fzd2.

DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz_domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 3.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G-PROTEIN RECEPTOR FZ 4; 1.
 DR Multigene family; G-PROTEIN COUPLED RECEPTOR; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 570
 FT DOMAIN 29 570
 FT DOMAIN 29 570
 FT TRANSMEM 253 273
 FT TRANSMEM 274 284
 FT TRANSMEM 285 305
 FT TRANSMEM 306 332
 FT TRANSMEM 333 353
 FT TRANSMEM 354 375
 FT TRANSMEM 376 396
 FT TRANSMEM 397 419
 FT TRANSMEM 420 440
 FT TRANSMEM 441 466
 FT TRANSMEM 467 487
 FT TRANSMEM 488 524
 FT TRANSMEM 525 545
 FT TRANSMEM 546 570
 FT DOMAIN 39 158
 FT DOMAIN 186 192
 FT DOMAIN 192 192
 FT SITE 548 553
 FT SITE 568 570
 FT CARBOHYD 58 58
 FT CARBOHYD 159 159
 FT CONFLICT 307 307
 SQ SEQUENCE 570 AA; 64058 MW; 79E7F71D10FC51A CRC64;
 E -> K (IN REF. 2).
 Query Match 36.3%; Score 476; DB 1; Length 570;
 Best Local Similarity 41.5%; Pred. No. 2.9e-30;
 Matches 107; Conservative 31; Mismatches 82; Indels 38; Gaps 10;
 Qy 2 APPDPAPSLLLILLIAQLVGRAPAAASKAPV-----COEITVPCRGIGVNLTHMPNQ 54
 Db 6 ALPRSLPRLPLLPLLLPAPGPAQGFGEKGISIPDHGFCQIPISIPICTDIAVYQTIMPL 65
 Qy 55 FHHDDDEAGLVHQPWVVEVQCSPDLAFPLCTWTPICLDYHKLPRPSCVCRARA 114
 Db 66 LGHTNDEAGLEVHQPWVVEVQCSPDLAFPLCTWTPICLDYHKLPRPSCVCRARA 124
 Qy 115 GCSPLMRQYGFAMPERMSCDRPLVGLRDAEVLCDMDYNRSE-----ATTAPRPFPAPKPT 168
 Db 125 GCEALMNKRGQFQWPERLREHFRHRC--AEQICVGNHSEDDAPALLTTAPPSGL--QRG 180
 Qy 169 LQPPGAPAPASGCECPAGG---PVCKCRBPVPLIKESHPLYNKRTGQVPCAVPCYQ 224
 Db 181 AGCTPGCGGCGSPRYATLEHFPICP-----RVLKV--PGLSYKFLGEBDCAPC-E 231
 Qy 225 PS-----FSADERTFA 235
 Db 232 PARPDGSMFFSQEETRFA 244

RESULT 10
 ID FZD2_RAT STANDARD; PRT; 570 AA.
 AC Q08464;
 DT 15-JUN-2002 (Rel. 41, Last created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 2 precursor (Frizzled-2) (Fz-2) (Fz2).
 GN FZD2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: High expression in adult skeletal muscle and
 CC fetal kidney, followed by fetal lung, adult heart, brain, and
 CC placenta. Specifically expressed in squamous cell esophageal
 CC carcinoma.

CC -1- DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).

CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).

CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.

CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

CC -----

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CC -----

DR EMBL; AB010881; BAA3424.1; -
 DR EMBL; AB017365; BAA3466.1; -
 DR Genbank; HGNC:4045; FZD7.
 DR MIM; 603410; -
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS00261; G-PROTEIN COUPLED RECEPTOR; Transmembrane;
 DR Multigene family; G-protein coupled receptor; Transmembrane;
 DR Developmental protein; Glycoprotein; Signal.
 DR SIGNAL; 1
 FT CHAIN; 33 574
 FT DOMAIN; 33 256
 FT TRANSMEM; 257 277
 FT DOMAIN; 278 288
 FT TRANSMEM; 289 309
 FT DOMAIN; 310 336
 FT TRANSMEM; 337 357
 FT DOMAIN; 358 379
 FT TRANSMEM; 380 400
 FT DOMAIN; 401 423
 FT TRANSMEM; 424 444
 FT DOMAIN; 445 470
 FT TRANSMEM; 471 491
 FT TRANSMEM; 492 528
 FT TRANSMEM; 529 549
 FT DOMAIN; 550 574
 FT DOMAIN; 574 637
 FT SITE; 552 557
 FT SITE; 572 574
 FT CARBOHYD; 63 63
 FT CARBOHYD; 164 164
 FT CONFLICT; 8 8
 FT CONFLICT; 15 15
 FT CONFLICT; 15 15

FT CONFLICT 201 201 K -> R (IN REF. 2).
 FT CONFLICT 308 308 F -> L (IN REF. 2).
 FT CONFLICT 408 408 F -> S (IN REF. 2).
 FT CONFLICT 415 415 F -> L (IN REF. 2).
 FT CONFLICT 433 433 F -> L (IN REF. 2).
 FT CONFLICT 447 447 F -> L (IN REF. 2).
 FT CONFLICT 534 534 C -> Y (IN REF. 2).
 FT CONFLICT 574 AA; 63/57 MW; BB868B9C2CFED42 CRC64;
 SQ SEQUENCE

Query Match 34.9%; Score 457; DB 1; Length 574;
 Beef Local Similarity 39.7%; Pred. No. 9e-29; Indels 46; Gaps 12;
 Matches 106; Conservative 34; Mismatches 81; Indels 46; Gaps 12;

QY 1 MARPPSAPPSTL---LTLAQLVGRRAAASRAP-----VCQBITVPKCRGI 44
 DB 1 MNDPGAAYVLSLGFCAVLTLALGALSAGAPHYNGKGISVPHGFCQPSISPLCTDI 60
 QY 45 GYNLTMPNQFNHDPDDEAGLEVQFWPLVEIQCSFDLRFPLCTMYTPICLPDHYKRLPP 104
 DB 61 AYNQITLPLVLTHTQEDAGLEVHQPYPVAVKQCSBELRFFLSMYAPVCTV-LDQAIIP 119
 QY 105 CRSVCERAKAGCSPLMROYGFAMPERMSCDRLPYIGRDAEVLQMDVNRSEATTAP--PR 161
 DB 120 CRSLCERARQGEALMNKGFQWPERKRCENFVHG--AGEICVGNISDGGSGGCGGFT 177
 QY 162 PPAKPTLPG-----PPGAPASGCECPAGCPVCKREPFYLIKESHPLNYKVTQGV 215
 DB 178 AVTPAAYVLDLFTLPLPG--ASDCKGRAPFPSC-RQLKXP-----PYIGYRLGE- 227
 QY 216 PNCVAIPCQPS-----FSADERTFA 235
 DB 228 RDCGAPC-EPGRANGIMYKKEERRFA 253

RESULT 12
 FZD7_MOUSE
 ID FZD7_MOUSE STANDARD; PRT; 572 AA.
 AC 061090;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 7 precursor (Frizzled-7) (Fz-7) (mz7).
 GN FZD7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96224032; PubMed=8626800;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
 RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.,
 RA "A large family of putative transmembrane receptors homologous to the
 RA product of the Drosophila tissue polarity gene frizzled.";
 RN J. Biol. Chem. 271:4468-4476(1996).
 RP [2]
 RP COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=99324445; PubMed=10395542;
 RA Sheidahl L.C., Park M., Malbon C.C., Moon R.T.;
 RA "Protein kinase C is differentially stimulated by Wnt and Frizzled
 RA homologs in a G-protein-dependent manner.";
 RL Curr. Biol. 9:695-698(1999).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity

CC information during tissue morphogenesis and/or in differentiated
 CC tissues. Activation by Wnt8 induces expression of beta-catenin
 CC target genes.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U43320; AAC52432.1; -
 CC MGI: 108570; Fzd7.
 CC InterPro: IPR000539; Frizzled.
 CC InterPro: IPR000024; Fz_domain.
 CC InterPro: IPR000832; GPCR_secretin.
 CC Pfam: PF01392; Fz_1.
 CC Pfam: PF01334; Frizzled; 1.
 CC PRINTS: PRO00489; FRIZZLED.
 CC SMART: SM00063; FRI; 1.
 CC PROSITE: PS50038; FZ; 1.
 CC PROSITE: PS50261; G-PROTEIN RECEPTOR_F2_4; 1.
 CC Multigene family; G-protein coupled receptor; Transmembrane;
 CC Developmental protein; Glycoprotein; Signal.
 CC SIGNAL 1 32
 CC CHAIN 33 572
 CC FT DOMAIN 33 254
 CC FT TRANSMEM 255 275
 CC FT DOMAIN 276 286
 CC FT TRANSMEM 287 307
 CC FT DOMAIN 308 334
 CC FT TRANSMEM 335 355
 CC FT DOMAIN 356 377
 CC FT TRANSMEM 378 398
 CC FT DOMAIN 399 421
 CC FT TRANSMEM 422 442
 CC FT DOMAIN 443 468
 CC FT TRANSMEM 469 489
 CC FT TRANSMEM 490 526
 CC FT TRANSMEM 527 547
 CC FT DOMAIN 548 572
 CC FT TRANSMEM 573 633
 CC FT SITE 570 572
 CC FT CARBOHYD 63 63
 CC FT CARBOHYD 164 164
 CC SQ SEQUENCE 572 AA; 63816 MW; 35A68079AC786DF5 CRC64;
 CC
 CC Query Match 33.6%; Score 440.5; DB 1; Length 572;
 CC Best Local Similarity 38.8%; Pred. No. 1.7e-27;
 CC Matches 100; Conservative 36; Mismatches 75; Indels 47; Gaps 12;

OY 171 GPGAPASGCECPAG-----PFVCKREPFVPLIKESHPLYNKVRGQVNCVAPCYQ 224
 DB 187 DPPTFAMS-----PSDCGRSLSPFSCP-RQLKVP-----PLYGRFLGE-RDCGAPC-E 233
 OY 225 PS-----FSADERTFA 235
 DB 234 PGRANGLMYKEERERFA 251
 CC
 CC RESULT 13
 CC FZD2_XENLA STANDARD; PRT; 551 AA.
 CC ID FZD2_XENLA
 CC AC Q9P0U6;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Frizzled 2 precursor (Frizzled-2) (Fz-2) (Xfz2).
 CC GN FZ2.
 CC OS Xenopus laevis (African clawed frog).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC OC Xenopodinae; Xenopus.
 CC OX NCBI_TaxId=8355;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Head;
 CC RX MEDLINE=99425192; PubMed=10495293;
 CC RA Deardorff M.A., Klein P.S.;
 CC RT "Xenopus frizzled-2 is expressed highly in the developing eye, otic
 CC vesicle and somites".
 CC RL Mech. Dev. 87:229-233 (1999).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed, especially in the eye
 CC anlage, otic vesicle and developing somites.
 CC -1- DEVELOPMENTAL STAGE: Minimal expression in oocytes and embryos
 CC prior to mid-blastula transition. Readily detected in the
 CC presumptive tissue from late gastrulae. By neurula stages, somitic
 CC expression is broader and also appears in developing neural
 CC structures and other anterior structures (eye anlage). By late
 CC neurula, the posterior expression is condensed into two stripes on
 CC each side, expression in the anterior tissues remains high in the
 CC developing eye. During tailbud stages, expression is still high in
 CC the eye vesicle, otic vesicle and other anterior regions, as well
 CC as the presumptive mesoderm. In the tadpole, highly expressed in
 CC the head, eye and otic vesicle, branchial arches and midportion of
 CC the somites.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -----
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CC or send an email to license@ib-sib.ch).
CC -----
CC EMBL: AF139165; AAF06359.1; -
CC InterPro: IPR000539; Frizzled.
CC InterPro: IPR000024; Fz domain.
CC InterPro: IPR000832; GPCR_secretin.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF01394; Frizzled; 1.
CC PRINTS: PR00469; FRIZZLED.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; Fz; 1.
CC PROSITE: PS50261; G-PROTEIN COUPLED RECEPTOR; Transmembrane;
CC Multigene family; G-protein coupled receptor; Transmembrane;
CC Developmental protein; Glycoprotein; Signal.
CC SIGNAL 1 26
CC CHAIN 27 551 FRIZZLED 2.
CC DOMAIN 27 231 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 232 252 1 (POTENTIAL).
CC TRANSMEM 253 285 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 266 286 2 (POTENTIAL).
CC TRANSMEM 287 313 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 314 334 3 (POTENTIAL).
CC DOMAIN 335 356 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 357 377 4 (POTENTIAL).
CC TRANSMEM 378 400 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 401 421 5 (POTENTIAL).
CC TRANSMEM 422 447 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 448 468 6 (POTENTIAL).
CC TRANSMEM 469 505 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 506 526 7 (POTENTIAL).
CC TRANSMEM 529 534 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 535 551 FZ.
CC SITE 529 534 LYS-THR-X-X-X-TRP MOTIF.
CC SITE 549 551 PDZ-BINDING.
CC CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 551 AA: 62461 MW: 3F29F168B8E6E007 CRC64;

Query Match 33.5%; Score 438.5; DB 1; Length 551;
Best Local Similarity 41.6%; Pred. No. 2.4e-27;
Matches 99; Conservative 29; Mismatches 73; Indels 37; Gaps 10;

QY 12 LLLLLLQVVG-RAAAASAPVCOEITVPMCRGIGNLTHMNOFHDQDAGLEVHQF 70
DB 16 LPTLSIGQHGKSGISVPHGFCQIPISIPLCDIAVNGTIMPLVLTQEDAGLEVHQF 75
QY 71 WFLVLEQCSPDRLRFELCTMYTPICLDYHKPLPRGSGVGERAKAGSPLMRQGFAMPER 130
DB 76 YFLVAVQCSSELRFLCSMYAPVCTV-LEQALPRCSICERAHGGEALMNKFGFQWPER 134
QY 131 MSCDRLPVLGRDAEVLCDMYNRSE-----ATTAPRPFPAPKPTLLGPPGAPASGECPA 184
DB 135 LAGCENPRRG--AEQICVGOINSESDGPTLLTSPH-----HGTCQPPV---YATL 181
QY 185 GGPVCKCKEPVPLIKESHPLYNKVRGQVNCAPVCQPS-----PSADERTFA 235
DB 182 DHPFHP-----RVLKV--PSYLNRFLEKDCAPC-EPTKSDGFMEFSGQEIRIFA 230

RESULT 14
FZD1_CHICK STANDARD; PRT; 592 AA.
AC 057328; Q91A07;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 1 precursor (Frizzled-1) (Fz-1) (cfz-1).
GN FZD1 OR FZ1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb bud;
RX MEDLINE=98260739; PubMed=9598377;
RA Kengaku M., Twombly V., Tabin C.;
RT "Expression of wnt and frizzled genes during chick limb bud
RT development.";
RL Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).
RN [2]
RP SEQUENCE OF 307-592 FROM N.A.
RX MEDLINE=20245319; PubMed=10781956;
RA Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;
RT "Characterization of avian frizzled genes in cranial placode
RT development.";
RL Mech. Dev. 93:195-200(2000).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins, inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated
CC tissues.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in the lens, otic placode (medial
CC wall of the vesicle) and in epibranchial placode. Also expressed
CC in the developing somites (dermyotome).
CC -1- DEVELOPMENTAL STAGE: Somites and placodal expression appears at
CC stage 9. At this stage, more obvious expression is detected in the
CC neural tube (midbrain and rostral hindbrain), and persists through
CC about stage 15. Strongly expressed in the ectoderm and around the
CC otic placodes at stage 12. At stage 16, otic expression declines,
CC expression in epibranchial placodes begins and peaks at stage 20.
CC Expression in the lens of the eye is first seen at about stage 15,
CC more evident at stage 16. At stage 17, seen in the ectoderm and
CC mesenchyme of the limb primordia. Detected at stage 20 in the lip
CC of the optic cup, in the mesenchyme surrounding the eye, in the
CC ectoderm overlying the lens and in the ectoderm caudal and ventral
CC of the olfactory placodes. From stages 20-30, expressed in
CC cartilage and in the dermyotomes and migrating scleromal cells
CC forming vertebrate.
CC -1- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ib-sib.ch).
CC -----
CC EMBL: AF031830; AAB87968.1; -
CC EMBL: AF224314; AAF61094.1; -
CC InterPro: IPR000539; Frizzled.
CC InterPro: IPR000024; Fz domain.
CC InterPro: IPR000832; GPCR_secretin.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF01534; Frizzled; 2.
CC PRINTS: PR00469; FRIZZLED.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; Fz; 1.
CC PROSITE: PS50261; G-PROTEIN RECEPTOR_FZ_4; 1.

```

KW Multigene family; G-protein coupled receptor; Transmembrane;
 KM Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 48
 FT CHAIN 49 592
 FT DOMAIN 49 271
 FT TRANSMEM 272 232
 FT TRANSMEM 293 303
 FT TRANSMEM 304 324
 FT TRANSMEM 325 351
 FT TRANSMEM 352 372
 FT TRANSMEM 373 394
 FT TRANSMEM 395 415
 FT TRANSMEM 416 438
 FT TRANSMEM 439 459
 FT TRANSMEM 460 485
 FT TRANSMEM 486 506
 FT TRANSMEM 507 546
 FT TRANSMEM 547 567
 FT TRANSMEM 568 592
 FT TRANSMEM 65 184
 FT SITE 570 575
 FT SITE 590 592
 FT CARBOHYD 84 84
 FT CARBOHYD 185 185
 FT CARBOHYD 533 533
 SQ SEQUENCE 592 AA; 65490 MW; 933E76063CA6109D CRC64;
 Query Match 32.9%; Score 431; DB 1; Length 592;
 Best Local Similarity 39.1%; Pred. No. 1e-26;
 Matches 99; Conservative 31; Mismatches 89; Indels 34; Gaps 8;
 QY 6 PSAPSLILLILL-----AQLVGRRAAASAPV-----COETVPMCRGIGYNTL 49
 DB 27 PRRPPLILLILLMAALPAGCGPAPAGPALSIRGISIPDHGCGPISIPCLTDIAVNOT 86
 QY 50 HNPNGNNDTODEAGLBNHOFWPLVEIQSPDIRFLCTMYTPTCLPDYKPLPPCRSVC 109
 DB 87 IMENLLGHTNQEAGLEVHGFYLVKQCAELKFLCSMYAVACTV-LEQALPPCRSLC 145
 QY 110 ERKACGSPIMROGFWAMPBRMSCDRLPYVGRDAEYLCMVYNSSEATTAPRRFPKPTL 169
 DB 146 ERRKQCEBALMNFQWPTLCKEKPVG--AGELCVQNSSEKTPPALRPESWT- 202
 QY 170 PGPPGAPASGECPPAGPFVCKCEKPEFVPLIKESHPLYNKRTGOVNCAPCYOPS--- 226
 DB 203 ---SNPHGCGGAGSGGPGARGRFSCPRALKV--PSYLNRYFLGEDGCAFC-FEGRLY 255
 QY 227 ---FSADERTFA 235
 DB 256 GLMYFGPEELRFS 268
 RESULT 15
 FZD1_MOUSE STANDARD; PRT; 642 AA.
 ID FZD1_MOUSE
 AC 070421; 008974;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fz1zled 1 precursor (Fz1zled-1) (Fz-1) (mFz1).
 GN FZD1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Embryo;
 RX MEDLINE=21233588; PubMed=11334716;
 RA Xu L., Tan L., Goldring M.B., Olsen B.R., Li Y.;
 RT "Expression of frizzled genes in mouse costochondral chondrocytes";
 RL Matrix Biol. 20:147-151 (2001).
 RN (2)

RP SEQUENCE OF 302-376 FROM N.A.
 RC TISSUE=Prostate;
 RA Johnson M.A., Greenberg N.M.;
 RL Submitted (May-1997) to the EMBL/Genbank/DBD databases.
 CC - FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - TISSUE SPECIFICITY: Expressed in chondrocytes.
 CC - DOMAIN: Lys-thr-X-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC - DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC - SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC - SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL; AF054623; AAC12873.2; -
 CC EMBL; AF005202; AAC01952.1; -
 CC MGD; MG1:1196625; Fz1.
 CC InterPro: IPR000539; Frizzled.
 CC InterPro: IPR000024; Fz domain.
 CC InterPro: IPR000832; GPCR_secretin.
 CC Pfam; PF01392; Fz; 1.
 CC PRINTS; PF01534; Frizzled; 2.
 CC SMART; SM00063; FRI; 1.
 CC PROSITE; PS50261; G_PROTEIN_RECPT_FZ_4; 1.
 CC PROSITE; PS50261; G-protein coupled receptor; Transmembrane;
 CC Multigene family; G-protein coupled receptor; Signal.
 CC Developmental protein; Glycoprotein; Signal.
 CC SIGNAL 1 68
 CC CHAIN 69 642
 CC DOMAIN 69 317
 CC TRANSMEM 318 338
 CC TRANSMEM 339 349
 CC TRANSMEM 350 370
 CC TRANSMEM 371 397
 CC TRANSMEM 398 418
 CC TRANSMEM 419 440
 CC TRANSMEM 441 461
 CC TRANSMEM 462 484
 CC TRANSMEM 485 505
 CC TRANSMEM 506 531
 CC TRANSMEM 532 552
 CC TRANSMEM 553 593
 CC TRANSMEM 594 614
 CC TRANSMEM 615 642
 CC TRANSMEM 106 225
 CC DOMAIN 85 90
 CC SITE 620 625
 CC SITE 640 642
 CC CARBOHYD 125 125
 CC CARBOHYD 226 226
 CC CONFLICT 341 341
 CC
 CC FRIZZLED 1.
 CC EXTRACELLULAR (POTENTIAL).
 CC 1 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 2 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 3 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 4 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 5 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 6 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 7 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC FZ.
 CC POLY-PRO.
 CC LYS-THR-X-X-X-TRP MOTIF.
 CC PDZ-BINDING.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC P -> R (IN REF. 2).

FT	CONFLICT	352	352	S -> F (IN REF. 2).
SQ	SEQUENCE	642 AA;	70955 MW;	0AAD0C0DC820B6CE CRC64;

SQ SEQUENCE 642 AA; 70955 MW; 0AAD0C0DC820B6CE CRC64;

Query Match	32.2%	Score 422;	DB 1;	Length 642;
Best [local] similarity	36.0%	Pred. NO 5	4e-26.	

Matches 102; Conservative 32; Mismatches 87; Indels 62; Gaps 10,

Matches 102; Conservative 32; Mismatches 87; Indels 62; Gaps 10,

```

QY      3 RDDPAPPSLLLL------AQLVGRAA--ASKAP-----31
Db      44 RADPRRMASSGLLLMLLEAPLLLLGLVRRQAAGVSGPQQQAPPPQQSQQYNBGRG1 1030
QY      32 -----VQGEITVPMCRGIGYNLTMPNQFNHDODEAGLEVHFWPLVEIQSPDLRF 85
Db      104 SIPDHGYCPISIPLCITMANQOTIMPTLLGHTNOEDAGLEVHOFYPLVKKQCSAEIKPF 163
QY      86 LCTMTPTICLPDYNHPTLPPCRSVCERAAAGCSPLMRQYGFAMPBMSCDRLPYLGRDAEV 145
Db      164 LCSMTAPCTV--LBAALTPCRSLCERAAQSGEALMNKFGFMPTLCKEKPVHG--AGE 220
QY      146 LCMIDNRSEATTAPRPAPKPTLLGPPGADASGGECPAG-----GPVCKCEPVP1 199
Db      221 LCVGQNTSDKGPPTPSLLPEFTWISGQHGGGGYRGVGGAGTVERGKFSCP--RALRPS 279
QY      200 LKESHPLYNKRVQGVNCAVCPQPS-----FSADERTFA 235
Db      280 YLYNHFLGEK-----DCGAPC--EPTLYGLMTFGPEELRFS 314

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Db 44 RADPRWASGLLLWLLEAPLLLGVRAGAGVSGPGQAPPPPPQPGSGQYNGEGI 103

32 -----VCOEITVPMCRGICYNLTHMPNQFNHDTQDEAGLEVHQEWPLVEIQCSPLRFF 85

Db 104 SIPDHGYCQPIISIP LCTDMAYNOTIMP NLLGHTNOEDAGLEVHOFYPLVKVQCSAE LKRF 1633

86 LCTMYTPICLPDYHKELPPCRSVCEERAKAGCSPLMROYGFAMPERNSCDRLPVLGRDAEV 145

164 1CSWA BYCTY-1.EQAL.PBCPSI.CEPABOCCEAI.MUKCEGOWBDTI.KCEKEPDYUC--JCE 320

[illegible]

146 LCMIDINKSEATIAEPKPLTPGPGAPASGCECPAG-----GPFVCKCREPIVPI 199

Db 221 LCVGQNTSDKGTPTPSLLPEFWTSNGQHGGGGRGGYPGGAGTVERKXFS^{CP}-RALRVPS 279

QY 200 LKESHPYLNKVRTGQVPCNCAPCYQPS-----FSADERTFA 235

Search completed: May 19, 2003, 16:34:31
Job time : 16 secs

Job time : 16 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 16:33:07 ; Search time 33 Seconds
(without alignments)
1467.305 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPPSAPSLLLLLAQL.....PNCAPVCQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MNC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_RODENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	801	61.1	579	13 Q9Y100	Q9Y100 brachydanio
2	801	61.1	579	13 Q9W6E4	Q9W6E4 brachydanio
3	800	61.1	579	13 Q9PTT7	Q9PTT7 brachydanio
4	796	60.8	592	13 Q9W6E2	Q9W6E2 brachydanio
5	794	60.6	576	13 Q9Y149	Q9Y149 brachydanio
6	794	60.6	576	13 Q9PWK6	Q9PWK6 brachydanio
7	794	60.6	576	13 Q9PMN8	Q9PMN8 brachydanio
8	461	35.2	574	4 Q96B74	Q96B74 homo sapien
9	451	34.4	550	5 Q9U8U6	Q9U8U6 caenorhabdi
10	429.5	32.8	550	13 Q9Y17	Q9Y17 brachydanio
11	426	32.5	872	5 Q9N145	Q9N145 ciona intes
12	410.5	31.3	559	13 Q90ZT3	Q90ZT3 brachydanio
13	408.5	31.2	559	13 Q98S12	Q98S12 brachydanio
14	403	30.8	557	13 Q8QFM3	Q8QFM3 brachydanio
15	401.5	30.6	591	4 Q8TAN2	Q8TAN2 homo sapien
16	380.5	29.0	577	13 Q918V7	Q918V7 brachydanio

17	379	28.9	315	13 Q91A95	Q91A95 gallus gall
18	367.5	28.1	319	13 P79993	P79993 xenopus lae
19	367	28.0	323	11 Q91W58	Q91W58 mus musculus
20	366.5	28.0	511	5 Q95X97	Q95X97 caenorhabdi
21	366.5	28.0	519	5 Q95X96	Q95X96 caenorhabdi
22	366.5	28.0	580	13 Q9PTT8	Q9PTT8 brachydanio
23	366.5	28.0	580	13 Q9W6E3	Q9W6E3 brachydanio
24	366.5	28.0	580	13 Q90WM3	Q90WM3 brachydanio
25	360	27.5	318	13 P79936	P79936 xenopus lae
26	359.5	27.4	315	13 Q9W6E0	Q9W6E0 brachydanio
27	347.5	26.5	348	11 Q35222	Q35222 rattus norv
28	347	26.5	351	11 Q9Z1N6	Q9Z1N6 mus musculus
29	340.5	26.0	303	11 Q9Z4N2	Q9Z4N2 rattus norv
30	339.5	25.9	148	11 Q91ZX9	Q91ZX9 mus musculus
31	339.5	25.9	568	5 Q91A29	Q91A29 caenorhabdi
32	338.5	25.8	346	4 Q14877	Q14877 homo sapien
33	338.5	25.8	348	11 Q9JLS5	Q9JLS5 rattus norv
34	326	24.9	197	11 Q9ULS4	Q9ULS4 rattus norv
35	322	24.6	213	13 Q9PTD9	Q9PTD9 gallus gall
36	320	24.4	545	5 Q9U322	Q9U322 hydra atten
37	317	24.2	130	6 Q95J81	Q95J81 cryctolagus
38	308	23.5	537	4 Q8TAV8	Q8TAV8 homo sapien
39	293	22.4	138	13 Q9PTM5	Q9PTM5 gallus gall
40	288.5	22.0	920	5 Q9SP13	Q9SP13 strongyloce
41	283.5	21.6	292	13 Q91A96	Q91A96 gallus gall
42	282	21.5	706	4 Q8WXR9	Q8WXR9 homo sapien
43	279	21.3	314	11 Q9WU66	Q9WU66 mus musculus
44	278.5	21.3	295	11 Q35297	Q35297 mus musculus
45	278.5	21.3	295	11 P97299	P97299 mus musculus

ALIGNMENTS

Q9Y100	1	PRELIMINARY;	PRT;	579 AA.	
AC	Q9Y100;				
DT	01-MAY-1999 (TREMBLrel. 10, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Frizzled 8a protein.				
GN	FZ8A.				
OS	Brachydanio rerio (zebrafish) (zebra danio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;				
OC	Cyprinidae; Danio.				
OK	NCBI_TaxID=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=OREGON;				
RX	MEDLINE=99077702; PubMed=9858730;				
RA	Kim S.H., Park H.C., Yeo S.Y., Hong S.K., Choi J.W., Kim C.H.,				
RA	Weinstein B.M., Huh T.L.;				
RT	"Characterization of two frizzled homologues expressed in the				
RT	embryonic shield and prechordal plate of zebrafish embryos";				
RL	Mech. Dev. 78:193-201(1998).				
DR	EMBL; AF060697; AAD05435.1; -				
DR	ZFIN; ZDB-GENE-000328-3; fZ8a.				
DR	InterPro; IPR000539; Frizzled.				
DR	InterPro; IPR000832; Fz domain.				
DR	Pfam; PF01534; Frizzled; I.				
DR	Pfam; PF01392; Fz; 1.				
DR	PRINTS; PRO0469; FRIZZLED.				
DR	SMART; SM00063; FRI; 1.				
DR	PROSITE; PS50038; Fz; 1.				
DR	PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.				
SO	SEQUENCE 579 AA; 65249 MW; AFSACG626A4EC06 CRC64;				
Query Match	61.1%;	Score 801;	DB 13;	Length 579;	
Best Local Similarity	63.1%;	Pred. No. 3e-69;			
Matches 147;	Conservative 25;	Mismatches 45;	Indels 16;	Gaps 6;	

```

QY 13 LLLLLLQVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNOFNHDTODEAGLEVHQFMP 72
DB 10 LFLALALPRSSGTTAKETICQEIYAVPLCKGIGYNTYMPNQFNHDTODEAGLEVHQFMP 69
QY 73 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAPWPRMS 132
DB 70 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAPWPRMR 129
QY 133 CDBLPVLGRDAEVLCDMNYNSEATTAP---RP--FPAKPTLP-----GPPG-APASGGE 181
DB 130 CDLLPVOGA-PDITLMDYNTDSTTVSPVLSKPTNYSKAINPHKKSGRGVGPNNKMP 188
QY 182 CPAGGFVCKCRPEFVILKESHPLYNKRVGTQVPCAVPCYQPSFSADERTF 234
DB 189 CERG-----CQCRAPMVPVNSDRHPLYNRVKVGQIPNCAMPCHNPFYTOBERTF 237

```

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RESULT 2
Q9W6E4 PRELIMINARY; PRT; 579 AA.
ID 09W6E4;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Frizzled protein.
GN FZ5.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Furutani-Seiki M.;
RT "Cloning and functional analysis of zebrafish frizzled genes.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF117389; AAD25359.1; -.
DR EMBL; AF117389; AAD25359.1; Frizzled.
DR InterPro; IPR000539; Frizzled.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF01534; Frizzled; 1.
DR PRINTS; PR00489; FRIZZLED.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
SQ SEQUENCE 579 AA; 65299 MW; 6388F61A2EC8C192 CRC64;

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Query Match 61.1%; Score 801; DB 13; Length 579;
Best Local Similarity 63.1%; Pred. No. 3e-69;
Matches 147; Conservative 25; Mismatches 45; Indels 16; Gaps 6;
QY 13 LLLLLLQVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNOFNHDTODEAGLEVHQFMP 72
DB 10 LFLALALPRSSGTTAKETICQEIYAVPLCKGIGYNTYMPNQFNHDTODEAGLEVHQFMP 69
QY 73 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAPWPRMS 132
DB 70 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAPWPRMR 129
QY 133 CDBLPVLGRDAEVLCDMNYNSEATTAP---RP--FPAKPTLP-----GPPG-APASGGE 181
DB 130 CDLLPVOGA-PDITLMDYNTDSTTVSPVLSKPTNYSKAINPHKKSGRGVGPNNKMP 188
QY 182 CPAGGFVCKCRPEFVILKESHPLYNKRVGTQVPCAVPCYQPSFSADERTF 234
DB 189 CERG-----CQCRAPMVPVNSDRHPLYNRVKVGQIPNCAMPCHNPFYTOBERTF 237

```

```

RESULT 3
Q9PTT7 PRELIMINARY; PRT; 579 AA.
ID 09PTT7

```

```

AC Q9PTT7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Frizzled homolog.
GN FZC OR ZFZC.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Hyatt T.M., Walsh E.E., Guttman J.R., Ekker S.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF039412; AAF21645.1; -.
DR ZFIN; ZDB-GENE-000210-30; FzC.
DR InterPro; IPR000539; Frizzled.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF01534; Frizzled; 1.
DR Pfam; PF01392; Fz; 1.
DR PRINTS; PR00489; FRIZZLED.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
SQ SEQUENCE 579 AA; 65265 MW; 5E84372126A4EA20 CRC64;

```

```

Query Match 61.1%; Score 800; DB 13; Length 579;
Best Local Similarity 63.1%; Pred. No. 3.7e-69;
Matches 147; Conservative 24; Mismatches 46; Indels 16; Gaps 6;
QY 13 LLLLLLQVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNOFNHDTODEAGLEVHQFMP 72
DB 10 LFLALALPRSSGTTAKETICQEIYAVPLCKGIGYNTYMPNQFNHDTODEAGLEVHQFMP 69
QY 73 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAPWPRMS 132
DB 70 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAPWPRMR 129
QY 133 CDBLPVLGRDAEVLCDMNYNSEATTAP---RP--FPAKPTLP-----GPPG-APASGGE 181
DB 130 CDLLPVOGA-PDITLMDYNTDSTTVSPVLSKPTNYSKAINPHKKSGRGVGPNNKMP 188
QY 182 CPAGGFVCKCRPEFVILKESHPLYNKRVGTQVPCAVPCYQPSFSADERTF 234
DB 189 CERG-----CQCRAPMVPVNSDRHPLYNRVKVGQIPNCAMPCHNPFYTOBERTF 237

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```

RESULT 4
Q9W6E2 PRELIMINARY; PRT; 592 AA.
ID 09W6E2;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Frizzled protein.
GN FZ2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Furutani-Seiki M.;
RT "Cloning and functional analysis of zebrafish frizzled genes.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF117387; AAD25357.1; -.
DR EMBL; AF117387; AAD25357.1; Frizzled.
DR InterPro; IPR000539; Frizzled.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF01534; Frizzled; 1.

```

DR Pfam: PF01392; Fz; 1
 DR PRINTS; PRO0489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PSS0038; Fz; 1.
 DR PROSITE; PSS0261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 592 AA; 66420 MW; E06CB4D19A9BD5E CRC64;

Query Match 60.8%; Score 796; DB 13; Length 592;
 Best Local Similarity 67.9%; Pred. No. 9, 3e-69;
 Matches 152; Conservative 17; Mismatches 51; Indels 4; Gaps 4;

QY 12 LLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPNHDTODEAGLEHQM 71
 DB 24 LHVLLFQSLGSDSASKIVCEPIVPMCKGIGYNHTMPNPNHNDODEVLEHVFWM 83
 QY 72 PLVEIQCSPDLRFELCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLMRQYGFAMPERN 131
 DB 84 PLVRHICSDLLFELCSMTPTICLDYKKPLPCRSVCERAKAGCSPLMQLYFEMPERM 143
 QY 132 SCDRLPVLGRDAEVLCDYNRSEATTAPPPAPKPTLPQPGAPASGCECPAGG-PFVC 190
 DB 144 SCQQLPMLG-DTQRLCMDNRSEETTLSP-PFP-KPTPKGTPRHATYAKSAPQKCDRC 200
 QY 191 KCSEPFVPIKESHPLYNKRTGOVNCAPCYQPSFSADERTF 234
 DB 201 HCGPLVPIKKAHPLNRYNTGSLPNCALPCHPYFSQDERTF 244

RESULT 5

QY149 PRELIMINARY; PRT; 576 AA.

AC QY149; PRELIMINARY; PRT; 576 AA.
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Frizzled homolog.
 GN ZFZA.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxId=7955;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98428612; PubMed=9753682;
 RA Naessvichus A., Hyatt T., Kim H., Guttman J., Walsh E., Sunamas S.,
 Wang Y., Ekker S.C.;
 RT "Evidence for a frizzled-mediated wnt pathway required for zebrafish
 RT dorsal mesoderm formation."
 RL Development 125:4283-4292(1998).
 DR EMBL; AF039410; AAC83940.1; -
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PRO0489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PSS0038; Fz; 1.
 DR PROSITE; PSS0261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 576 AA; 64911 MW; 996DB82FC5B47C8A CRC64;

Query Match 60.6%; Score 794; DB 13; Length 576;
 Best Local Similarity 63.5%; Pred. No. 1, 4e-68;
 Matches 148; Conservative 22; Mismatches 47; Indels 16; Gaps 4;

QY 7 SAPPSLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPNHDTODEAGLE 66
 DB 11 SALALCVLLLMSSVCGR-----EHVCOEISVPLCRGIGYNHTMPNPNHNDODEAGLE 64
 QY 67 VHQFWPLVEIQCSPLRFLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLMRQYGA 126
 DB 65 VHQFWPLVEIQCSPLRFLCTMYTPICLPDYKKPLPCRSVCERAKAGCAPLMRQYGP 124

QY 127 WPERNSCDRLPVLGRDAEVLCDYNRSEATTAPPP-----PPAKPTLPQPGAPASGCEC 182
 DB 125 WDRMRCDLLPYQG-DPNTLCMDYNRDATSSPAAPKTTSRGCKPFKRNKSSPSSSCE 183
 QY 183 PAGGFVCKCRFPFPIKESHPLYNKRTGOVNCAPCYQPSFSADERTFA 235
 DB 184 PE-----CYCRAPMVVPHSDHPLNRYNTGQIPNCAMPCHPYLSQEBRTFA 231

RESULT 6

QYPMK6 PRELIMINARY; PRT; 576 AA.

AC QYPMK6; PRELIMINARY; PRT; 576 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Frizzled 8b protein.
 GN FZ8B.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxId=7955;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON;
 RX MEDLINE=99077702; PubMed=9858730;
 RA Kim S.H., Park H.C., Yeo S.Y., Hong S.K., Choi J.W., Kim C.H.,
 Weinstein B.M., Huh T.L.;
 RT "Characterization of two frizzled homologues expressed in the
 RT embryonic shield and prechordal plate of zebrafish embryos."
 RL Mech. Dev. 78:193-198(1998).
 DR EMBL; AF060696; AAD17520.1; -
 DR ZFIN; ZDB-GENE-000328-4; fz8b.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PRO0489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PSS0038; Fz; 1.
 DR PROSITE; PSS0261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 576 AA; 64945 MW; 9965128DCDD1EDB8A CRC64;

Query Match 60.6%; Score 794; DB 13; Length 576;
 Best Local Similarity 63.5%; Pred. No. 1, 4e-68;
 Matches 148; Conservative 22; Mismatches 47; Indels 16; Gaps 4;

QY 7 SAPPSLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPNHDTODEAGLE 66
 DB 11 SALALCVLLLMSSVCGR-----EHVCOEISVPLCRGIGYNHTMPNPNHNDODEAGLE 64
 QY 67 VHQFWPLVEIQCSPLRFLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLMRQYGA 126
 DB 65 VHQFWPLVEIQCSPLRFLCTMYTPICLPDYKKPLPCRSVCERAKAGCAPLMRQYGP 124
 QY 127 WPERNSCDRLPVLGRDAEVLCDYNRSEATTAPPP-----PPAKPTLPQPGAPASGCEC 182
 DB 125 WDRMRCDLLPYQG-DPNTLCMDYNRDATSSPAAPKTTSRGCKPFKRNKSSPSSSCE 183
 QY 183 PAGGFVCKCRFPFPIKESHPLYNKRTGOVNCAPCYQPSFSADERTFA 235
 DB 184 PE-----CYCRAPMVVPHSDHPLNRYNTGQIPNCAMPCHPYLSQEBRTFA 231

RESULT 7

QYPMN8 PRELIMINARY; PRT; 576 AA.

AC QYPMN8; PRELIMINARY; PRT; 576 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE Frizzled protein.
 GN FZ6.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Furutani-Seiki M.
 RT "Cloning and functional analysis of zebrafish frizzled genes."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF117390; AAD25360.1; -
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.
 SQ SEQUENCE 576 AA; 64940 MW; F57E75B18629B9B6 CRC64;

Query Match 60.6%; Score 794; DB 13; Length 576;
 Best Local Similarity 63.5%; Pred. No. 1,4e-68;
 Matches 148; Conservative 22; Mismatches 47; Indels 16; Gaps 4;

QY 7 SAPPSLLILLAQLVGRAAAASAPVCOETITVPMCRGIGINTLHMPNQFNHDTODEAGLE*66
 DB 11 SALALCVLLIMSSVCGR-----EHVCOEISVPLCRGIGINTYMPNQFNHNDQENKLE 64
 QY 67 VHOFPMLVEIQCSPPDLRFELCTMYTPICLPDYHKPLPPCRSVCERAAAGCSPLMROYGFA 126
 DB 65 VHOFPMLVEIQCSPPDLRFELCTMYTPICLPDYHKPLPPCRSVCERAAAGCSPLMROYGFP 124
 QY 127 WPERMSCDRLPVLGRDAEVLCDMYNRSEATTAPRP----FPAKPTLPGPGAPASGSEC 182
 DB 125 WPDRLMCDLLPVGQ-DPNTLCMDYNRDATTSPAPAKRTSRPGKPFRRKKSSPGSSSCE 183
 QY 183 PAGPFPYCKREPPVPLKESHPLYNKVRGQVNCAPCYQSFSADEETFA 235
 DB 184 PE-----CYCRAPMVVPSHDHPLYNKVKGTGQIPNCAMPCHNPYLSQERTFA 231

RESULT 8
 ID Q96B74 PRELIMINARY; PRT; 574 AA.
 AC Q96B74;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Frizzled (Drosophila) homolog 7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015915; AAH15915.1; -
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.

SQ SEQUENCE 574 AA; 63620 MW; 801934246B426DF5 CRC64;
 Query Match 35.2%; Score 461; DB 4; Length 574;
 Best Local Similarity 40.1%; Pred. No. 2,3e-36;
 Matches 107; Conservative 33; Mismatches 81; Indels 46; Gaps 12;

QY 1 MARPPSAPPS---LILLLIQLVGRAAAASAPVCOETITVPMCRGIGINTLHMPNQFNHDTODEAGLE*66
 DB 1 MRDPGAAPLSSIGLCALVIALGLASAGAQPYHGEKGISVDPHGFQCPISIPICTDI 60
 QY 45 GYNLTMPNQFNHDTODEAGLEHOFVFWPLVEIQCSPPDLRFELCTMYTPICLPDYHKPLRP 104
 DB 61 ANQNTLLPMLHGTNOEDAGLEHOFVFWPLVEIQCSPPDLRFELCTMYTPICLPDYHKPLRP 119
 QY 105 CSVCERAAAGCSPLMROYGFAWPERMSCDRLPVLGRDAEVLCDMYNRSEATTAP---PR 161
 DB 120 CRLSCLRRAGCGEALMNKRGFQWPERLRNCPVNG--AGELCVQGNISDSGGPGCGPT 177
 QY 162 PEPKPTLPG-----PGAPASGGECPAGSPVCKREPPVPLKESHPLYNKVRGQV 215
 DB 178 AVPTAPYLLPDLPTALPPG--ASDGRGRPAFPFSCP-RQLKYP-----PYLGYRFLGE- 227
 QY 216 PNCVAPCYOPS-----FSADERTFA 235
 DB 228 RDCGAPC-EPGRANGLMYPKEERRFA 253

RESULT 9
 ID Q9U8U6 PRELIMINARY; PRT; 550 AA.
 AC Q9U8U6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, last annotation update)
 DE CFZ2.
 GN CFZ2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodertinae; Caenorhabditis.
 OC NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94429803; PubMed=10498678;
 RA Sato A., Kojima T., U-Irei K., Miyata Y., Saigo K.;
 RT "Frizzled-3, a new Drosophila mnt receptor, acting as an attenuator
 of Wingleless signaling in wingless hypomorphic mutants."
 RL Development 126:4421-4430 (1999).
 DR EMBL; AB026113; BAA84678.1; -
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.
 SQ SEQUENCE 550 AA; 62012 MW; 652968A853B1A69A CRC64;

Query Match 34.4%; Score 451; DB 5; Length 550;
 Best Local Similarity 38.9%; Pred. No. 2,1e-35;
 Matches 93; Conservative 31; Mismatches 77; Indels 38; Gaps 6;

QY 11 SLILLLIQLVGRAAAASAPVCOETITVPMCRGIGINTLHMPNQFNHDTODEAGLEHOF 70
 DB 6 SYLFLILGSC--GALFGRKQCEQITLPLCKGIGYNNMTSPNSYGHEKQEBAGLEHOF 62
 QY 71 WPLVEIQCSPPDLRFELCTMYTPICLPDYHKPLPPCRSVCERAAAGCSPLMROYGFAWPR 130
 DB 63 YPLVEVGCFQHLKFLCTMYTPICOENYDKPLPCLMELCVEARSKCSPIKARYGFRWPR 122

QY 131 MGCRLPVLGRDAEVLCDMNYNSSEATTAPRPPAKP-----TLPG 171
 DB 123 LSCBALPKMS-----DOMSTGNICAAAPDPKPKKHGHHKNNONONNNHNSPDG 174
 QY 172 PP-GAASAGSECPAG-GPFVCKGREPFVPLIKESHPLVNNKRTGOVPCAVPCQSFSS 228
 DB 175 PEVGIKIDNEVIAGSECCQCTCNQPFQVASE-----KSKVGNVNCAYSCHSPALA 227

RESULT 10

Q90YL7 PRELIMINARY; PRT; 550 AA.
 AC Q90YL7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Frizled-2.
 GN ZF22.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21369720; PubMed=11477686;
 RA Sumnas S., Kim H.J., Hermanson S., Ekker S.C.;
 RT "Zebrafish frizled-2 morphant displays defects in body axis elongation."
 RL Genesis 30:114-118(2001).
 DR EMBL; AF03592; AAK56401.1;
 DR InterPro; IPR000539; Frizled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizled; I.
 DR Pfam; PF01392; Fz; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 DR PROSITE; PS50038; Fz; 1.
 SQ SEQUENCE 550 AA; 61748 MW; 7F7A4C92B8E8AAE4 CRC64;

Query Match 32.8%; Score 429.5; DB 13; Length 550;
 Best Local Similarity 45.1%; Pred. No. 2.5e-33;
 Matches 87; Conservative 24; Mismatches 57; Indels 25; Gaps 8;

QY 33 COEITVPMCRGIGYNLTTHMPNCFHDTODAGLEVHQFMPLVIEIQSPDLRFCTMTYTP 92
 DB 39 CQPTITPLCTDIAYNOTIMPNLVGHYNQEDAGLEVHQFPLVAVQSPDLKFLCSMTYAP 98
 QY 93 ICLPDYHKLPLPCRSVCERAKAGCSPLMRQYGFAMPERMSCDRLPVLGDAEVLCDMNYN 152
 DB 99 VCTV-LEKAIPLPCRSICERAKAGCEVLMNKFGFQWPEALRCEHPVLG-DGHI-CVGQND 155
 QY 153 SEATTAPR-PPPAKT--LPGPAPASGSECPAGPFVCKGREPFVPLIKESHPLYNK 209
 DB 156 SWATVSPVMPFPGTSPVLYSTPDKP--RCPS-----TLKV-PAYLS 196
 QY 210 VRTGVPCAVPC 222
 DB 197 YKFLGEPDGCAPC 209

RESULT 11

Q9NL45 PRELIMINARY; PRT; 872 AA.
 AC Q9NL45;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Frizled homolog.
 GN CIFR2.
 OS Clona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Clonidae; Clona.

OK NCB1_TaxID=7719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imai K., Takada N., Satch N., Satch Y.;
 RT "An essential role of beta-catenin in the endoderm specification of ascidian embryo."
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB031542; BAA92184.1;
 DR InterPro; IPR000539; Frizled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizled; I.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZLED.
 DR SMART; SMO0063; FRI; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 872 AA; 96568 MW; 980E086E6E0D269C CRC64;

Query Match 32.5%; Score 426; DB 5; Length 872;
 Best Local Similarity 40.3%; Pred. No. 8.8e-33;
 Matches 98; Conservative 30; Mismatches 77; Indels 38; Gaps 12;

QY 9 PPSLLILLALQVGRAAASKAPVCOEITVPMCRGIGYNLTTH--PNQFNHDTODAGLE 66
 DB 112 PP-----ISGLSGRCGTG---VCEPIQVPMCIDIGVFTMSVPSYTD-QKEAAS 160
 QY 67 VHQFMPLVIEIQSPDLRFCTMTYTPICLPDYHKLPLPCRSVCERAKAGCSPLMRQYFA 126
 DB 161 VIOGFPPLTKCAEEMKLVCSVTPTICPGYGFPLPGRPFICEAKAGCEPILKKTNT 220
 QY 127 WPERMSCDRLP-VLGRDAEVLCDMNYNSEATTAP--PPPPAK--PTLGPAGA----- 175
 DB 221 WNLFLFCQKFPDSQGNPP--CLHFNRS-ATEEPAPRITTKGSKTTPGAPVASVTH 277
 QY 176 ---PASGCECPAGPFVCKGREPFVPLIKESHPLVNNKRTGOVPCAVPCQSFSSADR 232
 DB 278 PYKPLNG--CP-----CACARMKVITWKDPLVGVKVTGGVPCAMCPKSPFSEER 329

RESULT 12

Q90ZT3 PRELIMINARY; PRT; 559 AA.
 AC Q90ZT3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Frizled 7b.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Emeljanov A., Sleptsova-Friedrich I., Fong I., Korzh V.;
 RT "Frizled 7b interacts with Wnt5 in the enveloping layer of embryonic zebrafish."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF336123; AAK49948.1;
 DR InterPro; IPR002086; Aldhyde_dehydr.
 DR InterPro; IPR000539; Frizled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizled; I.
 DR Pfam; PF01392; Fz; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

SQ SEQUENCE 559 AA; 63695 MW; 85667E255AA50DB2 CRC64;
 Query Match 31.3%; Score 410.5; DB 13; Length 559;
 Best Local Similarity 41.8%; Pred. No. 1.7e-31;
 Matches 81; Conservative 25; Mismatches 65; Indels 23; Gaps 4;

QY 33 CQETIVPMCRGIGYNTLHMNPQNHDTQDAGLEVHOFMWFLVEIQSPDLRFELCTMYTP 92
 DB 45 CQETISPLCTDIAYNQITMNLGHTNQEDAGLEVHOFYFLVKVQCSMDLKFELCSMYAP 104
 QY 93 ICLPDHKLPLPCRSYVCERAKGCSPLMRQYGFAMPERMSCDRLPVLGRDAEVLCDMDYR 152
 DB 105 VCTV-LEQAIPLPCRSYVCERAKGCEALMKNKFGQWPERLRCENFPVHG--AGETCVGQNT 161
 QY 153 SEATTAPRRFPFAKPTL---PGPPGAPASGCECPAGFPVCKCRBEFVPLIKESHPLYN 208
 DB 162 SDAGSPTSNPTFYVPELITLQPNLVVRPNQOFTCP-----LQLKVPITYL 205
 QY 209 KVRTGOVPCNAVPC 222
 DB 206 KYHFMGKDCGAPC 219

RESULT 13
 ID 098S12 PRELIMINARY; PRT; 559 AA.
 AC 098S12;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Frizzled 7 protein (Fragment).
 GN FZ7.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=21184123; PubMed=11287199;
 RA El-Messaoudi S., Renucci A.;
 RT Expression pattern of the frizzled 7 gene during zebrafish embryonic
 RT development.";
 RL Mech. Dev. 102:231-234 (2001).
 DR EMBL: AJ301617; CAC3735.1;
 DR InterPro: IPR002086; Aldehyde_dehydr.
 DR InterPro: IPR000539; Frizzled.
 DR InterPro: IPR000824; Fz domain.
 DR Pfam: PF01534; Frizzled; 1.
 DR Pfam: PF01392; Fz; 1.
 DR PRINTS: PR00489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE: PS50038; FZ; 1.
 DR PROSITE: PS50261; G_PROTEIN_RECPT_F2_4; 1.
 FT NON TER 1
 SQ SEQUENCE 559 AA; 63719 MW; 25F243A465F04D4B CRC64;

Query Match 31.2%; Score 408.5; DB 13; Length 559;
 Best Local Similarity 41.8%; Pred. No. 2.7e-31;
 Matches 81; Conservative 25; Mismatches 65; Indels 23; Gaps 4;

QY 33 CQETIVPMCRGIGYNTLHMNPQNHDTQDAGLEVHOFMWFLVEIQSPDLRFELCTMYTP 92
 DB 45 CQETISPLCTDIAYNQITMNLGHTNQEDAGLEVHOFYFLVKVQCSMDLKFELCSMYAP 104
 QY 93 ICLPDHKLPLPCRSYVCERAKGCSPLMRQYGFAMPERMSCDRLPVLGRDAEVLCDMDYR 152
 DB 105 VCTV-LEQAIPLPCRSYVCERAKGCEALMKNKFGQWPERLRCENFPVHG--AGETCVGQNT 161
 QY 153 SEATTAPRRFPFAKPTL---PGPPGAPASGCECPAGFPVCKCRBEFVPLIKESHPLYN 208

DB 162 SDAGSPTSNPTFYVPELITLQPNLVVRPNQOFTCP-----LQLKVPITYL 205
 QY 209 KVRTGOVPCNAVPC 222
 DB 206 KYHFMGKDCGAPC 219

RESULT 14
 ID 080FM3 PRELIMINARY; PRT; 557 AA.
 AC 080FM3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Frizzled-7A.
 GN FZ7A.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
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 RX Sumana S., Kim H.J., Hermanson S.B., Ekker S.C.;
 RA "Zebrafish frizzled-7A is expressed maternally and zygotically during
 RT embryogenesis.";
 RT Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Emejanov A., Sleptsova-Friedrich I., Fong I., Korzh V.;
 RT "Frizzled 7b interacts with Wnt5 in the enveloping layer of embryonic
 RT zebrafish.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF437316; AA187635.1;
 DR EMBL: AF336124; AA00192.1;
 SQ SEQUENCE 557 AA; 63475 MW; DEF32BF11596C83 CRC64;

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 Best Local Similarity 41.0%; Pred. No. 9.2e-31;
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 QY 93 ICLPDHKLPLPCRSYVCERAKGCSPLMRQYGFAMPERMSCDRLPVLGRDAEVLCDMDYR 152
 DB 105 VCTV-LEQAIPLPCRSYVCERAKGCEALMKNKFGQWPERLRCENFPVHG--AGETCVGQNT 161
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 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Primates; Catarrhini; Homiidae; Homo.
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 RX TISSUE=BRIN;

RA Strusberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
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Best Local Similarity 37.4%; Pred. No. 1,4e-30; Indels 33; Gaps 7;

Matches 89; Conservative 28; Mismatches 88; Indels 33; Gaps 7;

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 DB 10 LLLMQLLAGGALLEGREFDPERGRGAPQAVETPMCRGIGYNLTMRNLGHTSGEA 69
 QY 64 GLEVHOFWPLVEIQSPDLRFELCTMYTPICLPDYHKPLPPCRSVCEAKAGCSPLMRQY 123
 DB 70 AAELAEFAFLVQYGGCHSHLRFELCSLYAPMCTDQVSTPIPACRPMCEQARLRCAPIMEQF 129
 QY 124 GFAMPBRMSCDRLPVLRGDAEVLQMDYNRSEATTAPRP-----FPAKPTLPGPRGAPA 177
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Search completed: May 19, 2003, 16:35:38
 Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 22, 2003, 21:24:29 ; Search time 2664 Seconds
(without alignments)
2567.252 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARDPSPAPSLLLLAQL.....FNCAVPCYQSPFSADERTFA 235

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2054640 seqs, 14551402878 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1250	95.4	179788	2 AC101915	AC101915 Mus muscu
5	1143	87.3	1734	10 AF272146	AF272146 Mus muscu
6	1131.5	86.4	746	9 HS4329758	AJ329758 Homo sapi
7	1017	77.6	821	9 HS433422	AJ333422 Homo sapi
8	832.5	63.5	2380	5 AF300716	AF300716 Xenopus 1
9	824	62.9	2085	6 AX367099	AX367099 Sequence
10	824	62.9	3195	9 AB043703	AB043703 Homo sapi
11	824	62.9	166007	9 HSB4425A6	AL121749 Human DNA
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14	802	61.2	1851	5 AF017177	AF017177 Xenopus 1
15	801	61.1	1740	5 AF117389	AF117389 Dario rer
16	801	61.1	2249	5 AF060697	AF060697 Dario rer
17	800	61.1	2554	5 AF039412	AF039412 Dario rer
18	796	60.8	1779	5 AF117387	AF117387 Dario rer
19	796	60.8	3230	5 AF033110	AF033110 Xenopus 1
20	794	60.6	1731	5 AF117390	AF117390 Dario rer
21	794	60.6	2522	5 AF060696	AF060696 Dario rer
22	794	60.6	2523	5 AF039410	AF039410 Dario rer
23	621	47.4	2085	3 DMU65589	U65589 Drosophila
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25	621	47.4	180387	3 AC009378	AC009378 Drosophila
26	621	47.4	279530	3 AE003518	AE003518 Drosophila
27	543.5	41.5	62712	2 AC018167	AC018167 Drosophila
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29	479.5	36.6	2112	10 AF206321	AF206321 Mus muscu
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34	476	36.3	182182	2 AC091152	AC091152 Homo sapi
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36	461	35.2	3067	9 BC015915	BC015915 Homo sapi
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 REFERENCE 1 (bases 1 to 2334)
 AUTHORS Wang, Y., Macke, J.P., Abella, B.S., Andreasen, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J.
 TITLE A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled
 JOURNAL J. Biol. Chem. 271 (8), 4668-4476 (1996)
 MEDLINE 96224032
 PUBMED 8626800
 REFERENCES 2 (bases 1 to 2334)
 AUTHORS Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
 DIRECT SUBMISSION
 JOURNAL Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
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 Query Match: 100.00% Indels: 0
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 REFERENCE 1 (bases 1 to 3134)
 AUTHORS Saitoh, T., Hirai, M. and Katoh, M.
 TITLE Molecular cloning and characterization of human Frizzled-5 gene on chromosome 2q33.3-q34 region
 JOURNAL Int. J. Oncol. 19 (1), 105-110 (2001)
 MEDLINE 21301556
 PUBMED 1151251
 REFERENCES 2 (bases 1 to 3134)
 AUTHORS Katoh, M.
 DIRECT SUBMISSION
 JOURNAL Submitted (24-MAY-2000) Masaru Katoh, National Cancer Center, Genetics Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan (E-mail: mkatoh@cc.go.jp, Tel: 81-3-3542-2511 (ex. 4402), Fax: 81-3-3541-2685)
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US-09-847-102a-68 (1-235) x AB043702 (1-3134)

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JOURNAL
MEDLINE
PUBMED

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2 (bases 1 to 177733)
Belter,E., Cotton,M. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-801F7
Unpublished (2001)
3 (bases 1 to 177733)
Waterson,R.H.
Direct Submission
Submitted (25-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 177733)
Waterson,R.H.
Direct Submission
Submitted (14-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 177733)
Waterson,R.H.
Direct Submission
Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 177733)
Waterson,R.
Direct Submission
Submitted (23-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 14, 2002 this sequence version replaced gi:16604097.

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0801F07
Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Cacanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-196E10, 2000 bp overlap; the clone sequenced to the right is RP11-372C13, 2000 bp overlap. Actual end of this clone is at base position 22072 of RP11-372C13.

Polymorphisms have been identified between AC009409, AC079767, AC083900 and AC096772.

Data from AC009409 and AC022576 was used to finish this clone, AC096772.

FEATURES

The sequence of AC036191 has been incorporated into AC096772.

source Location/Qualifiers

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Query Match: 99.69% Indels: 0
DE: 9 Gaps: 0
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US-09-847-102a-68 (1-235) x AC096772 (1-177733)

[illegible]

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 179788)
 Batten, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Baetjen, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepiel, Y., Collimore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farkas, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamet, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Teeffaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, V., Zemek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 21, 2002 this sequence version replaced gi:117060691.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

 Center: Whitehead Institute/ MIT Center for Genome Research

 Center code: WtBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

 Project Information

 Center project name: L17740
 Center clone name: 388.P.13

 Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 170170 bases at least Q40
 Consensus quality: 174390 bases at least Q30
 Consensus quality: 176052 bases at least Q20
 Insert size: 170000; agarose-fp
 Insert size: 177888; sum-of-contigs
 Quality coverage: 4.9 in Q20 bases; agarose-fp
 Quality coverage: 4.7 in Q20 bases; sum-of-contigs

 NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 1 945: contig.f 945 bp in length

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* 946 1045: gap of 100 bp
* 1046 2264: contig of 1219 bp in length
* 2265 2364: gap of 100 bp
* 2365 3772: contig of 1408 bp in length
* 3773 3872: gap of 100 bp
* 3873 5301: contig of 1428 bp in length
* 5302 5401: gap of 100 bp
* 5402 6775: contig of 1374 bp in length
* 6776 6875: gap of 100 bp
* 6876 8156: contig of 1281 bp in length
* 8157 8256: gap of 100 bp
* 8257 9750: contig of 1494 bp in length
* 9751 9850: gap of 100 bp
* 9851 12095: contig of 2245 bp in length
* 12096 12195: gap of 100 bp
* 12196 15020: contig of 2825 bp in length
* 15021 15120: gap of 100 bp
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* 19029 19128: gap of 100 bp
* 19129 24573: contig of 5445 bp in length
* 24574 24673: gap of 100 bp
* 24674 32390: contig of 7717 bp in length
* 32391 32490: gap of 100 bp
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* 47517 47616: gap of 100 bp
* 47617 63562: contig of 15946 bp in length
* 63563 63662: gap of 100 bp
* 63663 79343: contig of 15681 bp in length
* 79344 79443: gap of 100 bp
* 79444 95603: contig of 16160 bp in length
* 95604 95703: gap of 100 bp
* 95704 110699: contig of 14996 bp in length
* 110700 110799: gap of 100 bp
* 110800 127693: contig of 16894 bp in length
* 127694 127793: gap of 100 bp
* 127794 143731: contig of 15938 bp in length
* 143732 143831: gap of 100 bp
* 143832 179788: contig of 35957 bp in length.
Location/Qualifiers
1. 179788

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Score: 1250.00 Matches: 224
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Best Local Similarity: 95.32% Mismatches: 7
Query Match: 95.42% Indels: 0
Dn: 2 Gaps: 0

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US-09-847-102a-68 (1-235) x AC101915 (1-179788)

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Db 20334 ATGGCTCAGCCGAGCCGCTGCGCTCCTCTTCTGCTGCTGCTGCGCAGCG 20393
Qy 21 ValGlyArgAlaAlaAlaSerLysAlaProValCysGlnGluIleThrValProMet 40
Db 20394 GTGGCCGAGGAGCGCGCGCTCCAGGCCCCGGGTGCCAGAAATACGCTGCCATG 20453
Qy 41 CysArgGlyIleGlyTyrAsnLeuThrIsmecProEnglnPheAsnHisAspThrGln 60
Db 20454 TGCCGAGGATCGGTACACTGACGACGACATGCCCAACGATTCAACATGACGACG 20513
Qy 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80
Db 20514 GACGAAGCAGCGCTGAGAGTGCACCAATTCGCGCTTGCGAGATCAGCTGCTCACCG 20573
Qy 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
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Qy 121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
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Qy 141 ArgAspAlaGluValLeuCysMetCaspTyrTrpAsnArgSerGluAlaThrThAlaProPro 160
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Qy 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
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LOCUS	AF272146	1734 bp	mRNA	linear	ROD 12-DEC-2000
DEFINITION	Mus musculus transmembrane receptor frizzled 5 (Fzd5) mRNA,				
ACCESSION	AF272146				
VERSION	AF272146.1				
KEYWORDS					
SOURCE	Mus musculus.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1734)				
TITLE	Ishikawa,T., Tamai,Y., Zorr,A.M., Yoshida,H., Selin,M.F., Nishikawa,S. and Takeo,M.M. Mouse Wnt receptor gene Fzd5 is essential for yolk sac and placental angiogenesis				
JOURNAL	development 128 (1), 25-33 (2001)				
MEDLINE	20545163				
PubMed	11092808				
REFERENCE	2 (bases 1 to 1734)				
AUTHORS	Ishikawa,T.-o., Tamai,Y. and Takeo,M.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-MAY-2000) Pharmacology, Kyoto University Graduate School of Medicine, Yoshida Konoe-cho, Sakyo-ku, Kyoto 606-8501, Japan				
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BASE COUNT	298 a	579 c	493 g	364 t	
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Alignment Scores:					
Pred. No.:	1.99e-59				1734
Score:	1143.00				Matches: 214
Percent Similarity:	92.34%				Conservative: 3
Best Local Similarity:	91.06%				Mismatches: 14
Query Match:	87.25%				Indels: 4
DB:	10				Gaps: 3
US-09-847-102A-68 (1-235) x AF272146 (1-1734)					
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Db	1	ATGGCTGACCCGACCCGCTGCGGCTCTCTCTCTCTGCGCTGCTGCGAGCTG	60		
Oy	21	ValGjAgaLaalaalaalaSerLysAlaProValCyGInGluLleThrValProMet	40		
Db	61	GTGGGCGGCGAGCGCGCTCCAGGCCCGCGGTGTCAGGAATACCGTGCATG	120		
Oy	41	CyaaRgGjYllEGlYTYaaNleuThriShiEcProaNGInPheAeNhiAaSPThGln	60		

Db	121	1GCCGAGGCGCATCGGCTACAACTGACGCCACATGCCCAACAGCTTCAACCATGACACGCG	180
Oy	61	AspGluAlaGlyLeuGluValAlHisGlnPheTrpProLeuValGluIleGlnCysSerPro	80
Db	181	GACCAAGACAGCGCTCGAGAGTGACCAATTCCTGCGCCGTTGTGGAGATCCACTGCTCACCG	240
Oy	81	AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisIlys	100
Db	241	GACCTGGCGCTCTTCCTGTGCTCATATGATACAGGCCCATCTGTGTCCTGATACACAAAG	300
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Oy	121	ArgGlnTyrGlyPheAlaIleTrpProGluArgMetSerCysAspArgLeuProValIleuGly	140
Db	361	CGCCAGTAGAGGCTTCGCTGGCCCGAGCGGATGAGTGCAGCCGCTCCCTGCTGGGC	420
Oy	141	ArgAspAlaGluValIleuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro	160
Db	421	GGCAGCGCGGAGGTTCGTGTGTATGATTATTAACGGAAGCGAA--ACCACCGCTCCCT	477
Oy	161	ArgProPheProAlaIysProThrLeuProGlyIleProGluAlaProAlaSerGlyGly	180
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Oy	181	GluCysProAlaGlyGlyProPheValCysIleCysArgGluProPheValProIleu	200
Db	538	GAGTGC---TCGGAGGTCACTCGTGTGCAGTGC-----GAGCCCTTCGTGCCATCTG	588
Oy	201	LysGluSerHisIleProLeuTyrAsnLysValArgThrGlyGluValProAsnCysAlaVal	220
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Oy	221	ProCysTyrGlnProSerSerPheSerAlaAspGluValArgThrPheAla	235
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RESULT 6

LOCUS HSA329758

DEFINITION Homo sapiens genomic sequence surrounding Not1 site, clone

ACCESSION AJ329758

VERSION AJ329758.1

KEYWORDS GI:15874176

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Kutsenko, A.S., Gizatulilin, R.Z., Al-Amin, A.N., Wang, F., Kvaeha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.

TITLE Not1 flanking sequences: a tool for gene discovery and verification of the human genome

JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)

PUBMED 12136098

REFERENCE 2 (bases 1 to 746)

AUTHORS Zabarovsky, E.R.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorphology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

FEATURES

source location/Qualifiers

1..746 /organism="Homo sapiens"

/db_xref="taxon:9606"

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BASE COUNT 119 a 271 c 216 g 140 t


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Db 448 GACTTACACCGCACCACTTACACCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCGCG 507
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Qy 166 LysProThrLeuProGly-----ProProGly 174
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RESULT 10
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DEFINITION complete cds.
ACCESSION AB043703
VERSION AB043703.1 GI:13623798
KEYWORDS Homo sapiens cDNA to mRNA, clone_lib:human fetal lung cDNA library
SOURCE (CLONTECH).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Saichon,T., Hirai,M. and Katoh,M.
TITLE Molecular cloning and characterization of human Frizzled-8 gene on

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JOURNAL chromosome 10p11.2
MEDLINE Int. J. Oncol. 18 (5), 991-996 (2001)
REFERENCE 21192958
AUTHORS 2 (bases 1 to 3195)
TITLE Katoh,M.
JOURNAL Direct Submission
SUBMITTED (24-MAY-2000) Masaru Katoh, National Cancer Center,
Genetics Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan
(E-mail:m.katoh@ncc.go.jp, Tel:81-3-3542-2511 (ex.4402),
Fax:81-3-3541-2685)
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Alignment Scores:
Pred. No.: 2.9e-40 Length: 3195
Score: 824.00 Matches: 161
Percent Similarity: 67.66% Conservative: 21
Best Local Similarity: 59.85% Mismatches: 39
Query Match: 62.90% Indels: 48
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US-09-847-102a-68 (1-235) x AB043703 (1-3195)
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 DEFINITION Human DNA sequence from clone RP11-425A6 on chromosome 10, complete
 sequence.
 ACCESSION AL121749
 VERSION AL121749.14 GI:21541283
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 166007)
 HEALTH P.
 DIRECT SUBMISSION
 Submitted (21-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Jun 23, 2002 this sequence version replaced gi:17530251.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr10
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk

 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. RP11-425A6 is from
 the library RPC1-11.2 constructed by the group of Pieter de Jong.
 For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: BAC3.6.
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ACCESSION		U43321	
VERSION		U43321.1	
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ORGANISM		Mus musculus.	
REFERENCE		Mus musculus.	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus. 1 (bases 1 to 2421)	
TITLE		Wang, Y., Macke, J. P., Abella, B. S., Andreasson, K., Mowley, P., Gilbert, D. J., Copeland, N. G., Jenkins, N. A. and Nathans, J., A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996)	
JOURNAL		66224032	
MEDLINE		8626800	
PUBMED			
REFERENCE		2 (bases 1 to 2421)	
AUTHORS		Abella, B., Wang, Y., Macke, J. P. and Nathans, J.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205	
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US-09-847-102A-68 (1-235) x MMU43321 (1-2421)	
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DEFINITION	pieces.
ACCESSION	AC108777
VERSION	AC108777.2 GI:21326315
KEYWORDS	HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Mus musculus, clone Rp23-368H22
AUTHORS Unpublished
REFERENCE 2 (bases 1 to 215585)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collingore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatae, A., Kelle, C., Larocque, K., Lamazares, R., Lander, E., Lenoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Struss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 215585)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collingore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatae, A., Kelle, C., Larocque, K., Lamazares, R., Lander, E., Lenoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Struss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (05-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE On Jun 5, 2002 this sequence version replaced g1:18450034.
COMMENT ALL repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L19221
Center clone name: 368_H22
----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 210679 bases at least Q40
Consensus quality: 212848 bases at least Q30
Consensus quality: 213560 bases at least Q20
Insert size: 225000; agarose-fp
Insert size: 21985; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; agarose-fp
Quality coverage: 9.4 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

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1571 1670: gap of 100 bp
1671 2309: contig of 639 bp in length
2310 2409: gap of 100 bp
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3289 4467: contig of 1179 bp in length
4468 4567: gap of 100 bp
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6723 6822: gap of 100 bp
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14622 14721: gap of 100 bp
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Percent Similarity: 69.06% Conservative: 24
Best Local Similarity: 60.00% Mismatches: 39
Query Match: 62.86% Indels: 43
Gaps: 8
US-09-847-102A-68 (1-235) x AC108777 (1-215585)
QY 11 SerLeuLeu-----LeuLeuLeuLeuAAGlnLeuValGlyArgAlaAlaAlaSer 28
Db 76201 TCGCTCTAGCGCGCTTGGCGGTGCTACAGCGCTACAGCGCGCTTGGCGGTGCGGC 76260
QY 29 LysAlaProValCysGlnGluLeuValPromeCysArgGlyIleGlyTyrAlaLeu 48
Db 76261 AAGGACCTGCGCGCAAGAGATCAGCGTCTGTGCAAGAGCATCGTTTACACTAC 76320
QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspAlaGlyLeuGluValHis 68
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QY 69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
Db 76381 CAGTTTGGCGCGTGTGAGATACAGTGTCTCCCGGACCTCAAGTTCTTGTGTAC 76440
QY 89 MetTyrThrProIleCysLeuProAspTyrHisLysProLeuProCysArgSerVal 108
Db 76441 AAGTACACCCCATCTGCTCGAGGACTACAAAGAACCTCTGCGCTTGTGCTGTG 76500
QY 109 CysGlnArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrPro 128
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QY 129 GlnArgMetSerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMet 148
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QY 149 AspTyrAsnArgSerGlnAlaThrThraA-----ProProArgProPheProAla 165
Db 76618 GACTACAAACCGCACCGACTCACAGCGCGCCACCGCACCGCGCGCTGTCCG 76677
QY 166 LysProThrLeuProGly-----ProProGly 174
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QY 176 ProAlaSerGlyGlyGluCys-----ProAlaGlyGlyProPheVal----- 189
Db 76795 CCTTGGCGCGGGGAGAGCGAGCGCCCTGTGCGCGCGCTGCTCTCGGAGCGGAG 76854
QY 190 CysLysCysArgGluProPheValProIleLeuLysGlnSerHisProLeuTyrAsnLys 209
Db 76855 TCCAGTCCCGCGCGCCCATGTGAGCTGTCCACGACACCGCCCTCTACACCGC 76914
QY 210 ValArgThrGlyGlnValProAsnCysAlaValProCysTyrGlnProSerPheSerAla 229
Db 76915 GTCAAGACCGGCGCAGATGCCCAACTGCTGCGCTGCGCTCCACACCCCTTTCAGCAG 76974
QY 230 AspGluArgThrPhe 234
Db 76975 GATGAGCGCGCTTC 76989
RESULT 14
AF017177 1851 bp mRNA linear VRT 11-AUG-1998
LOCUS AF017177
DEFINITION Xenopus laevis frizzled 8 protein (Xfz8) mRNA, complete cds.
ACCESSION AF017177
VERSION AF017177.1 GI:3123437
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 1851)
1 Itoh, K., Jacob, J. and Y. Sokol, S.
A role for Xenopus Frizzled 8 in dorsal development
Mech. Dev. 74 (1-2), 145-157 (1998)
21059883
MEDLINE
PUBMED
2 (bases 1 to 1851)
Itoh, K., Jacob, J. and Sokol, S. Y.
Direct Submission
Submitted (04-AUG-1997) Microbiology and Molecular Genetics,
Harvard Medical School and Beth Israel Deaconess Medical Center,
330 Brookline Ave., Boston, MA 02215, USA
FEATURES
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1..1851
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SIMWVLLTWFLAAGMGWBAIAGSYOYFHLAAMLVPSIKSIAVLALSSVDGPVA
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LMIRIGISVUTYTPATITVACFPYEGNRRNGEVAHKNCSQCBMAOPHPDVAFPM
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BASE COUNT 374 a 547 c 502 g 428 t
ORIGIN
Alignment Scores:
Pred. No.: 3.42e-39 Length: 1851
Score: 802.00 Matches: 149
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Qy      182 CysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeuLys 201
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Db      565 TCGGAGCCCGGGC-----TCCCACTGTGCGCGCGCGGATGCTGCCGCGTAACAGC 612
Qy      202 GluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaValPro 221
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      613 GATCGACACCGCGCTCTACCAACCGCGTTAAGACGCGGTCAAACTCCCAACTGCGCCATGCCA 672
Qy      222 CysTyrGlnProSerPheSerAlaAspGluArgThrPhe 234
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Db      673 TGTCAACACCAATATTATTACGCGAGATGAGCGGACTTTT 711
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Search completed: May 23, 2003, 05:26:08
Job time : 2758 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 18:42:08 ; Search time 263 Seconds
(without alignments)
2012.242 Million cell updates/sec

Title: US-09-847-102a-68

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	Fgapop 6.0	Fgapext 7.0
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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	2334	18 AAT89889	Human frizzled gen
2	824	62.9	2085	24 ABK15174	Human REPT1 6 cDNA
3	823.5	62.9	2421	18 AAT89892	Mouse frizzled gen
4	754	57.6	424	24 ABK83141	Human ovarian can
5	621	47.4	2085	23 ABK29961	Drosophila melanog
6	621	47.4	2344	18 AAT88885	Drosophila frizzle
7	621	47.4	4085	23 ABK28960	Drosophila melanog
8	440.5	33.6	2259	18 AAT88911	Mouse frizzled gen
9	415	31.7	1941	21 AAA60179	Hydrophobic domain
10	415	31.7	4485	21 AAA60189	Hydrophobic domain
11	398	30.4	4540	24 ABK63777	Rat sequence diffe
12	387	29.5	3269	22 AAF75974	Human frizzled fam
13	380.5	29.0	1909	19 AAV13101	Human hftz cDNA.
14	380.5	29.0	1909	24 ABK64750	Human benign prost
15	380.5	29.0	1909	24 ABK61945	Colon adenocarcino
16	378	28.9	1893	19 AAV14017	Human "frizzled" f
17	372.5	28.4	1484	19 AAV18254	Human growth-induc
18	372.5	28.4	1920	20 AAX28653	Nucleotide sequenc
19	372.5	28.4	1920	21 AAA40573	Xenopus sp embryo
20	372.5	28.4	2039	22 AAF80535	Receptor #3 parti
21	370.5	28.3	2621	22 AAF75973	Mouse frizzled fam
22	370	28.2	3847	23 ABK28857	Drosophila melanog
23	367.5	28.1	1291	19 AAV18255	Xenopus growth-ind
24	367.5	28.1	1786	19 AAV13102	Mouse hftz cDNA.
25	367.5	28.1	2441	19 AAV13104	Mouse hftz cDNA (v
26	367	28.0	2176	19 AAV14016	Mouse "frizzled" f
27	367	28.0	2176	24 ABK9691	Mouse ischaemic co
28	366	27.9	2374	19 AAV18253	Bovine growth-indu
29	360	27.5	1875	19 AAV14014	Xenopus "frizzled"
30	349	26.6	1969	20 AAX28658	Partial human FRAZ
31	349	26.6	1969	22 AAC84496	Partial nucleotide
32	349	26.6	1969	24 ABK88234	Human osteoblast d
33	349	26.6	5311	23 ABK28856	Drosophila melanog
34	342.5	26.1	1046	20 AAX28655	Nucleotide sequenc
35	342.5	26.1	1458	19 AAX28651	Human ATE-1639 pro
36	342.5	26.1	1581	19 AAX28656	Human FRAZ2LED pol
37	342.5	26.1	1767	22 AAC84495	Receptor #86 parti
38	342.5	26.1	2009	22 AAF80598	Bos taurus Frazzle
39	342	25.9	1041	21 AAA90657	Human FRAZ2LED pro
40	339.5	25.8	1041	21 AAA54128	Breast cancer prot
41	338.5	25.8	2830	24 ABK92118	Prostate cancer-as
42	338.5	25.8	2830	24 AAL41901	Human frizzled rel
43	338.5	25.8	2840	21 AAA54127	Breast cancer prot
44	338.5	25.8	2840	21 AAA54127	Human colorectal c
45	338.5	25.8	2840	21 AAA97364	

ALIGNMENTS

RESULT 1
AAT89889
ID AAT89889 standard: DNA; 2334 BP.

AC AAT89889;
XX
XX
DT 27-APR-1998 (first entry)
XX
XX
DE Human frizzled gene 5 (Hfz5) encoding a Wnt receptor.
XX Wnt receptor; human frizzled gene 5; Hfz5 gene;
KW signal transduction; cancer; cell growth; cell proliferation;
KW mammary tumour; oncogene; therapy; ds.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 321..2078

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FT      /tag= a
XX      WO9739357-A1.
XX      23-OCT-1997.
XX      11-APR-1997; 97WO-US06049.
XX      12-APR-1996; 96US-0015307.
XX      (UJJO ) UNIV JOHNS HOPKINS.
XX      (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI      Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
PI      Nussle R, Samos CH, Wangy;
XX
DR      WPI; 1997-526631/48.
DR      P-PSDB; AAW31271.
XX
PT      Identification of Wnt receptor binding modulators - useful for
PT      treatment of cancer and growth, development or proliferation related
PT      disorders
XX
PS      Disclosure, Page 36-37; 61pp; English.
XX
XX      This sequence comprises novel human frizzled gene 5 (Hfz5)
XX      CC that encodes a transmembrane receptor, frizzled-5 (see AAW31771), a
XX      CC Mnt receptor (WntR). Novel frizzled family members have been
XX      CC identified in Drosophila, mouse, human and Caenorhabditis (see
XX      CC AAT8885-92) and are considered to be Wnt receptors. Wnt receptors
XX      CC can be used in a novel, claimed method of screening for compounds
XX      CC which modulate the binding of a Wnt polypeptide (secreted proteins
XX      CC involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
XX      CC involved in (mammary) cancer and other processes involving growth,
XX      CC development and proliferation (both normal and abnormal).
XX      CC Modulators identified by the claimed method are useful for
XX      CC treatment of diseases related to these conditions.
XX
SQ      Sequence 2334 BP; 356 A; 803 C; 736 G; 439 T; 0 other;
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Pred. No.: 6,2e-84 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
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US-09-847-102A-68 (1-235) x AAT89889 (1-2334)
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OY      41 CysArgGlyTlIeGlyTyrTrsLeuLeuThrLysMetProAsnGlnPheAsnHisAspThrGln 60
DB      441 TCCCGCGGCGATCGCTGACCACTGACGACGACATGCCAAGCTTCAACACGACGACGAG 500
OY      61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlnIleGlnCysSerPro 80
DB      501 GACGAGCGGCGCGCTGAGGTGACCACTGCTGCGCGCTGTGTGAGATTCATCTCTGCGG 560
OY      81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
DB      561 GACCTGCGCTTCTTCTATGACATATGATACACCCCATCTGTGTGCCACATCACCAAG 620
OY      101 ProLeuProProCysArgSerValCysGluArgAlaAlaGlyCysSerProLeuMet 120
DB      621 CCGCTGCGCGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 680

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OY      121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValIleuGly 140
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OY      141 ArgAspAlaGluValLeuCysMetLaspTyrAsnLysSerGluAlaThrThrAlaProPro 160
DB      741 CGCGAGCGCGGAGGTCTCTGTGATGATTACACCGCAGCGAGGCCACACGCGCGCCCCC 800
OY      161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180
DB      801 AGGCTTTTCCAGCCAGCCAGCCAGCTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 860
OY      181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeu 200
DB      861 GAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 920
OY      201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnValAlaVal 220
DB      921 AAGGAGTACACCCCGCTCTACCAAGGTGCGAGCGCGCGCGCGCGCGCGCGCGCGGTA 980
OY      221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB      981 CCTGCTACACCGCGCTTCTTCACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1025

RESULT 2
ID      ABK15174
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XX
DT      23-APR-2002 (first entry)
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DE      Human REPTR 6 cDNA sequence.
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KW      antiviral; anti-HIV; antiarthritic; anticonvulsant; nootropic;
KW      neuroprotective; antiallergic; antibody; immunogen; endometriosis;
KW      gastrointestinal disorder; gastritis; oesophageal carcinoma;
KW      Crohn's disease; irritable bowel syndrome; ulcerative colitis;
KW      endocrine disorder; hypothalamus disorder; Kallman's disease;
KW      autoimmune disease; inflammatory disease; infertility; receptor;
KW      acquired immune deficiency syndrome; AIDS; rheumatoid arthritis;
KW      allergy; osteoarthritis; diabetes mellitus; multiple sclerosis;
KW      systemic lupus erythematosus; cell proliferative disorder;
KW      cancer; developmental disorder; Duchenne muscular dystrophy; gene;
KW      Becker muscular dystrophy; neurological disorder; epilepsy; receptor;
KW      Alzheimer's disease; Huntington's disease; reproductive disorder; SS.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 1..2085
FT      /tag= a
FT      /product= "REPTR6 protein"
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XX      WO200198354-A2.
XX
PD      27-DEC-2001.
XX
PF      21-JUN-2001; 2001WO-US19942.
XX
XX      21-JUN-2000; 2000US-214027P.
XX      25-AUG-2000; 2000US-228045P.
XX      12-DEC-2000; 2000US-255104P.
XX
PA      (INCY-) INCYTE GENOMICS INC.
XX
PI      Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
PI      Lal P, Policky JC, Azimzai Y, Lu DM, Graul R, Yao MG, Burford N;
PI      Hafalia Adu, Baughn MR, Bandman O, Paterson C, Yang J,
PI      Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Dugan BM, Lu Y;
XX

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DR MPI: 2002-090432/12.
 DR P-PSDB: AA074823.

PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
 PT the diagnosis, treatment and prevention of gastrointestinal (e.g.
 PT gastritis) autoimmune/inflammatory (e.g. osteoarthritis) and cell
 PT proliferative (e.g. cancer) disorders -

XX Claim 62; Page 146-147; 157pp; English.

CC This invention relates to twelve human receptor cDNA sequences
 CC referred to as REPTR-1 to REPTR-12), and the proteins encoded thereby.
 CC The proteins of the invention may have antiinflammatory, cytostatic,
 CC immunosuppressive, antiviral, anti-HIV, antiautistic, muscular active
 CC general, anticonvulsant, nootropic, neuroprotective, anti-allergic
 CC activities. The sequences of the invention may be used to produce REPTR
 CC agonists or antagonists, and the protein sequences may be used to raise
 CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and
 CC polypeptides of the invention are useful in the diagnosis, treatment and
 CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,
 CC Crohn's disease, irritable bowel syndrome, ulcerative colitis),
 CC endocrine (e.g. hypochalimus disorder, Kallman's disease), autoimmune/
 CC inflammatory (e.g. acquired immune deficiency syndrome (AIDS),
 CC rheumatoid arthritis, allergies, osteoarthritis, diabetes mellitus,
 CC multiple sclerosis, systemic lupus erythematosus), cell proliferative
 CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular
 CC dystrophy), neurological (e.g. epilepsy, Alzheimer's disease,
 CC Huntington's disease) and reproductive (e.g. infertility, endometriosis)
 CC disorders. Numerous other examples of each disorder are given in the
 CC specification. The present sequence represents the human REPTR6 cDNA
 CC sequence of the invention.

XX SO Sequence 2085 BP; 276 A; 737 C; 741 G; 331 T; 0 other;

Alignment Scores:

Pred. No.: 1,686-49 Length: 2085
 Score: 824.00 Matches: 161
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 Best Local Similarity: 59.85% Mismatches: 39
 Query Match: 62.90% Indels: 48
 DB: 24 Gaps: 8

US-09-847-102a-68 (1-235) x ABK15174 (1-2085)

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 DB 31 TCGGCTGCTGGCGCGCTTGGCGCTGCTGCGAGCGCTCTAGGCGGCGCGCGCTCGGCG 90
 QY 29 LysAlaProValCysGlnGlnLeuTherValPrometCysArgGlyIleGlyTyrAnLeu 48
 DB 91 AAGGAGCTGGCATGCCAAGAGATCAACCGCGCTGTGTGAAGGCGATCGGCTACAACTAC 150
 QY 49 ThrHisMetProAenGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGlnValHis 68
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 DB 211 CAGTCTCGCGCGCTGCTGAGATCCAGTCTCGCGCGATCTCAAGTCTCTCTGTCAGC 270
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 DB 271 ATGTACAGCGCCCATGTGCTTAGAGACTACAGAAAGCGCTCGCGCTCGGCG 330
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 DB 331 TCGGAGCGCGCGCGCGCGCTGCGCGCTCAGCGCGCTCAGCGCGCTCGCGCGCG 390
 QY 129 GlnArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMet 148
 DB 391 GACCGCATGCGCTGCGAGCGCGCTGCGCGCGAGAGCG---AACCCTGACACGCTGTGCATG 447
 QY 149 AspTyrAsnArgSerGlnAlaThrThrala-----ProProArgProPheProAla 165

DB 448 GACTACAAACCGCAGCGAGCTTAACACCGCGCCCGAGCGCGCGCGCTCGCGCG 507
 QY 166 LysProThrLeuProGly-----ProProGly 174
 DB 508 CCGCGG-----CCGCGAGACCGCGCTTCCGAGCGGCGCAGCGCGCGCGCGG 561
 QY 175 Ala----- 175
 DB 562 GCCAGCGCGCGCGCGCGCGCGCGCGAGGGCGGTGCGCGCGGAGCGCGCGCGCG 621
 QY 176 ProAlaSerGlyGly-----GlyCysProAlaGlyGlyProPheVal 189
 DB 622 CCAGCTCCGCGCGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCTCC 681
 QY 190 -----CysLysCysArgGlnProPheValProIleLeuLysGlySerHisPro 205
 DB 682 TCGGAGCGCGCGGTCCATGCTCGCGCGCTTGTGTGAGCGGTGTCCAGCGAGCGCA 741
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 DB 742 CTCTACACCGCGGTCAACAGACAGCGCGAGATCCCTAATCGCGCGCTGCGCAACACCC 801
 QY 226 SerPheSerAlaAspGlnArgThrPhe 234
 DB 802 TTTTTCACCGCAGCAGCGCGCGCTTC 828
 RESULT 3
 ID AAT89892 standard; DNA; 2421 BP.
 AC AAT89892;
 XX 27-APR-1998 (first entry)
 DT
 XX
 DE Mouse frizzled gene 8 (Mfz8) encoding a Wnt receptor.
 XX
 KW Wnt receptor; mouse frizzled gene 8; Mfz8 gene;
 KW signal transduction; cancer; cell growth; cell proliferation;
 KW mammary tumour; oncogene; therapy; de.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 188..2245
 FT /tag= a
 FT
 XX
 FN WO9739357-A1.
 XX
 PD 23-OCT-1997.
 PD
 XX
 PF 11-APR-1997; 97WO-US06049.
 PR
 XX 12-APR-1996; 96US-0015307.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
 PI Nusee R, Samos CH, Wangy;
 DR MPI: 1997-526631/48.
 DR P-PSDB: AAW31274.
 PT Identification of Wnt receptor binding modulators - useful for
 PT treatment of cancer and growth, development or proliferation related
 PT disorders
 XX
 PS Disclosure: Page 46-47; 61pp; English.
 CC This sequence comprises novel mouse frizzled gene 8 (Mfz8)
 CC that encodes a transmembrane receptor, frizzled-8 (see AAW31274),
 CC a Wnt receptor (WntR). Novel frizzled family members have been

CC identified in Drosophila, mouse, human and Caenorhabditis (see
 CC AAT89885-92) and are considered to be Wnt receptors. Wnt receptors
 CC can be used in a novel, claimed method of screening for compounds
 CC which modulate the binding of a Wnt polypeptide (secreted proteins
 CC involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
 CC involved in (mammary) cancer and other processes involving growth,
 CC development and proliferation (both normal and abnormal).
 CC Modulators identified by the claimed method are useful for
 CC treatment of diseases related to these conditions.

XX
 XX
 SQ Sequence 2421 BP; 403 A; 772 C; 779 G; 467 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2,15e-49	2421	159	24	39	43	8
Score: 823.50						
Percent Similarity: 69.06%						
Best Local Similarity: 60.00%						
Query Match: 62.86%						
DB: 18						

US-09-847-102a-68 (1-235) x AAT89892 (1-2421)

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QY 11 SerLeuLeu-----leuLeuLeuAaGlnLeuValGlyArgAaAaAaAaSer 28
DB 218 TGGCTCTAGCCGCGCTTGGCGGTGTACAGCGCTTACGCGCGCTTCCGCGCTTGGCC 277
QY 29 LysAlaProValCysGlnGluIleThrValProMetCysArgGlyIleGlyTYraLeu 48
DB 278 AAGGAGCTGGCGCGCCAGAGATCAGCGTCCCTTGCAAGAGCATCGGTTCACATC 337
QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGlnAaGlyLeuGluValHis 68
DB 338 ACTTACATGCCCAACAGATTCAACAGCACAGCAGCAGATGAGCGCGCTTACGAGTGCAC 397
QY 69 GlnPheThrProLeuValGluIleGlnCysSerProAspLeuAaRphPheLeuCysTrp 88
DB 398 CAGTTTGGCGCGTGTGAGATACAGTGTCTCCCGAGCTCAAGTTCTTCTGTGTAGC 457
QY 89 MetTYrThrProIleCysLeuProAspTYrHisLysProLeuProCysArgSerVal 108
DB 458 AATGACAGCCCATCTGCTGTGAGAGACTACAGAGCTTGTGCTGTGTGTGTGTGTGTG 517
QY 109 CysGluArgAlaLysAaGlyCysSerProLeuMetArgGlnTYrGlyPheAlaTrpPro 128
DB 518 TGTGAACGGCGCCAGAGCGCGCTGCGCGCTCATCGCCAGTACGCGCTTGTGTGCGCT 577
QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet 148
DB 578 GACCGCATGCGCTGCATCGTGTGCGGAGACAGGCG--AACCGGACACTCTGTGCATG 634
QY 149 AspTYrAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
DB 635 GACTACAAACCGACCGACCTCACCACGCGCGCCAGCCAGCCGCGCGCTGTCCG 694
QY 166 LysProThrLeuProGly-----ProProGly 174
DB 695 CCGCCTCTCT---CCCGGAGAGAGCGCCCTCTGAGAGGCGCACAGCCGCGCGAGG 751
QY 175 Ala----- 175
DB 752 GCCAGGCCCCACATCTGGCGGAGAGTAGGAGGAGCGCGGAGCGGCGCTGCGCCC 811
QY 176 ProAlaSerGlyGlyGlyCys-----ProAlaGlyGlyProPheVal----- 189
DB 812 CCTTCGCGGCGGAGAGGAGCGCGCCCTGTGTGTGCGCGCTCTCCCTGCGAGCGGGG 871
QY 190 CysLysCysArgGluProPheValProIleLeuLysGluSerHisProLeuTYrAsnLys 209
DB 872 TGCAGATGCGCGCGCCCATGTGTGAGCGGTGTCCAGGAAGCAGCAGCCGCTTACACCCG 931
QY 210 ValArgThrGlyGluValProAsnCysAlaValProCysTYrGlnProSerPheSerAla 229
DB 932 GTTCAGACCGCGCGCATGTGTGTGCGCTGCGCCACAACTTTCTTTAGCCAG 991

```

QY 230 AspGluArgThrPhe 234
 DB 992 GATGAGCGCGCGCTTC 1006

RESULT 4

ID ABL83141 standard; cDNA; 424 BP.

AC ABL83141;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:6119.

OS Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

XX WO200192581-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide; polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide

XX Claim 1; SEQ ID 6119; 489bp; English.

CC The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence

CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to

CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell

CC population of (III), or antigen presenting cells that express (II).

CC (II) has cytosolic activity. An oligonucleotide (IV) that hybridises to

CC (S1) can be used for detecting ovarian cancer in a patient's biological

CC sample preferably serum or ovarian tissue. The method comprises

CC contacting a biological sample from a patient with (IV), detecting the

CC amount of polynucleotide hybridising to (IV) and comparing the amount to

CC a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is

CC detected preferably by polymerase chain reaction (PCR). (I) comprising

CC (III) and/or (II) is useful for stimulating and/or expanding T cells

CC specific for an ovarian tumour protein comprising contacting T cells

CC with (III) or (II). (III) is useful in design and preparation of

CC ribozyme molecules for inhibiting expression of the tumour polypeptides

CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known

CC techniques.

XX
 XX
 SQ Sequence 424 BP; 71 A; 163 C; 123 G; 67 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2,63e-45	424	137	1	3	1	0
Score: 754.00						
Percent Similarity: 97.87%						
Best Local Similarity: 97.16%						
Query Match: 57.56%						
DB: 24						

US-09-847-102a-68 (1-235) x ABL83141 (1-424)


```

DB      874 CAAGATGCGCGCGCTCCCAACTGCGATCCCTGCAAGGCGCTTCTTCACCAAC 933
QY      230 AAGGUAIGThrPheAla 235
        |||||:|||||
        934 GACGAAAGATTCCGC 951

RESULT 6
AAT9885
ID      AAT9885 standard; DNA; 2344 BP.
XX
AC      AAT9885;
XX
DT      27-APR-1998 (first entry)
XX
DE      Drosophila frizzled gene 2 (Dfz2) encoding a Wnt receptor.
XX
KW      Wnt receptor; Drosophila frizzled gene 2; Dfz2 gene;
        wingless receptor; Wg receptor; signal transduction; cancer;
        cell growth; cell proliferation; mammary tumour; oncogene; ds.
XX
OS      Drosophila melanogaster.
XX
FH      Key
FT      CDS
        Location/Qualifiers
        146..228
        /tag= a
        /transl_except= (pos:944..946, aa:Gln)
        /transl_except= (pos:947..949, aa:Leu)
        /transl_except= (pos:1188..1189, aa:Xaa)
        /transl_except= (pos:1188..1189, aa:Leu)
        /note= "this codon has an apparent 1 nucleotide
        deletion, which alters the reading frame"
FT      /transl_except= (pos:1609..1611, aa:Phe)
FT      /transl_except= (pos:2028..2040, aa:Ala)
FT      /transl_except= (pos:2041..2043, aa:Leu)
FT      /transl_except= (pos:2155..2156, aa:Ala)
        /note= "this codon has an apparent 1 nucleotide
        deletion, which alters the reading frame"
XX
XX      MO9739357-A1.
XX
PD      23-OCT-1997.
XX
PF      11-APR-1997; 97WO-US06049.
XX
PR      12-APR-1996; 96US-0015307.
XX
PA      (UXTD ) UNIV JOHNS HOPKINS.
        (STRD ) UNIV IELAND STANFORD JUNIOR.
XX
PI      Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
        Nusse R, Samos CH, Wangy;
XX
DR      WPI: 1997-526631/48.
        P-PSDB; AAM31267.
XX
PT      Identification of Wnt receptor binding modulators - useful for
        treatment of cancer and growth, development or proliferation related
        disorders
XX
PS      Disclosure, Page 21-23; 61pp; English.
XX
CC      This sequence comprises the Drosophila frizzled gene 2 (Dfz2) that
        was identified as a receptor for wingless (Wg). To isolate the
        gene, degenerate PCR primers based on sequences (see AAM31275-76)
        conserved in Dfz1, human frizzled 3 (Hfz3), rat frizzled 1 (Rfz1)
        and rat frizzled 2 (Rfz2) were used to amplify genomic DNA, and the
        PCR product was used to isolate genomic clones of Dfz2 from an adult
        Drosophila genomic library. The Drosophila frizzled-2 protein (see
        AAM31267) acts as a signal transducing molecule for Wg, consistent
        with its being a receptor for Wg, and is an example of a Wnt
        receptor (WntR). Other novel frizzled family members have been
        identified in human, mouse and Caenorhabditis elegans (see
        AAT9886-92) and are also considered to be Wnt receptors. Wnt

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CC      receptors can be used in a novel, claimed method of screening for
CC      compounds which modulate the binding of a Wnt polypeptide (secreted
CC      proteins involved in cell-to-cell signalling) to a Wnt receptor.
CC      Wnt is involved in (mammary) cancer and other processes involving
CC      growth, development and proliferation (both normal and abnormal).
CC      Modulators identified by the claimed method are useful for
CC      treatment of diseases related to these conditions.
XX
SQ      Sequence 2344 BP; 469 A; 732 C; 705 G; 438 T; 0 other;

Alignment Scores:
Pred. No.:      4,87e-35      Length:      2344
Score:          621.00      Matches:      124
Percent Similarity: 52.80%      Conservative: 27
Best Local Similarity: 43.36%      Mismatches: 55
Query Match:    47.40%      Indels:      80
DB:              18      Gaps:      7

US-09-847-102A-68 (1-235) x AAT9885 (1-2344)
QY      22 GIYAGAlaAlaAlaSerlySAlaPro-----
DB      263 GGTCAAGCGCTCGAGCGGATCCCGCATCCCGGTTACGAGTCCAGCCATACCAAGAT 322
QY      32 -----ValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeu 48
DB      323 CCCAATCTCGCATGAGAGAGATACCATACCAATGTGCGGGCATTTGGCTTACAACATG 382
QY      49 ThrHsMetProAsnGlnPheHsHisAspThrGlnAspGluAlaGlyIleuGluValHis 68
DB      383 ACATCTTCTCCCAAGAAATGACATAGACATGACCCGAGAGCGGCGCTGAGGTGCAC 442
QY      69 GlnPheTyrProLeuValAlaGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
DB      443 CAGTTCTGCGCCCTGTGTGAGATCAATGCTGCCGAGCTCAATTTCTTCTGTGCAGC 502
QY      89 MetTyrThrProIleCysLeuProAspTyrHisIlyProLeuProCysArgSerVal 108
DB      503 ATGTACAGCGCCCATCTGCTGCGTGGAGATTACCAAGCCGCTGCCGTTGCGGAGTGC 562
QY      109 CysGluArgAlaAlaGlyCysSerProLeuMetArgIleTyrGlyPheAlaThrPro 128
DB      563 TCGGAGAGAGCCCGTCCGAGATCGACCCATCATGACAGCTTACAGCTTCGAATGGCG 622
QY      129 GluArgMetSerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMet 148
DB      623 GAGAGAAATGCGTGGAGACACTTGCCTTCATGT-----GACCCGACATGTGTGATG 679
QY      149 AspTyr-----
DB      680 GAACAGCCCTCGTACACGAGGCTGCGAGCGTGGCAGCTCGGCGGATCGGTTGCTCT 739
QY      150 -----
DB      740 GGCAGCGTTCGGCTCCGCGCGGCAACGAGAGAGAGCATGCTCGGCGCGCACT 799
QY      151 -----AsnArgSerGluIleThrThrAlaProProArgProPheProAlaIlys 166
DB      800 GGGGCGCGGAGAGAGCGGCTTCCACCTCAAGAGCGGCGGAGAGCAATTCATAA 859
QY      167 ProThrLeuProGlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGly 186
DB      860 ---AACTGCMAAATCCCAAGAGAAAAGCGAAGGAAAAGAGTGAGC----- 907
QY      187 PropheValCysGlyArgGluProPheVal----- 197
DB      908 -----TGCCTGTCGCGCTCCCTCACTCATCTTCTGGGAGAGAGCACTGCTGCAG 958
QY      198 -----ProIleuTyrGlnSerHisProLeuTyrAsnIleVal----- 210
DB      959 CAGCAGTGCAGATGCCATATGATGACCATTCACACCACTGTATATGAACCTCACTGTC 1018
QY      211 ---ArgThrGlyGlnValProAsnCysAlaValProCysTyrGlnProSerPheSerAla 229

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Db      1019 CAAAGATCGCCGGCTTCAACTGCGCATATCGTCAAGGGCCCTTTTCAGCAAC 1078
Qy      230 AepgluArgThrPheAla 235
        |||||
Db      1079 GACGAAAGGATTTGCC 1096

RESULT 7
ID      ABL29960 standard; DNA; 4085 BP.
XX      ABL29960;
AC      ABL29960;
DT      26-MAR-2002 (first entry)
DE      Drosophila melanogaster genomic polynucleotide SEQ ID NO 41353.
XX      Drosophila: developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ds.
XX      Drosophila melanogaster.
OS      Drosophila melanogaster.
FN      MO200171042-AZ.
XX      27-SEP-2001.
XX      23-MAR-2001; 2001WO-US09231.
XX      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.
PA      (PEKE) PE CORP NY.
XX      Venter JC, Adams M, Li PWD, Myers EW;
XX      WPI: 2001-656660/75.
XX      New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
XX      Claim 1; SEQ ID NO 41353; 21pp + Sequence Listing; English.
XX      The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (AB857737-AB872072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pcc_sequences.
XX      Sequence 4085 BP; 949 A; 1122 C; 1102 G; 912 T; 0 other;
SQ

Alignment Scores:
Pred. No.:      9.05e-35      Length:      4085
Score:          621.00      Matches:      124
Percent Similarity: 52.80%      Conservative: 27
Best Local Similarity: 43.36%      Mismatches:  55
Query Match:    47.40%      Indels:      80
DB:            23      Gaps:      7

US-09-847-102a-68 (1-235) x ABL29960 (1-4085)
Qy      22 GlyArgAlaAlaAlaSerIysAlaPro----- 31
        |||||
Db      1118 GGTCAAGCGCTGAGCGAGTCCGACCCGGTTACGAGNCGCAGTACATACCAAGAT 1177
        |||||
Qy      32 -----ValCysGlnGluIleThrValProMetCysArgGlyTlleglYTYrAnleu 48
        |||||

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Db      1178 CCCAATCTGCATGCGAGAGATCACCATACCAATGTCTCGGGGATTGGCTACACATG 1237
Qy      49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAepGluAlaGlyLeuGluValHis 68
        |||||
Db      1238 ACATCTTCCCCCAAGAAATGAACCATGAGACCCAGAGCGAAGCGGCTGGAGGTGCAC 1297
        |||||
Qy      69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
        |||||
Db      1298 CAGTTCTGCCCCCTGGTGGATCAAAATGCTCGCGGACCTCAAGTTCTTCTTGCGAGC 1357
        |||||
Qy      89 MetTYrThrProIleCysLeuProAspTYrHisIysPheProLeuProCysArgSerVal 108
        |||||
Db      1358 ATGTACACGCCCATCTGCTGAGGATTAACAACAAGCCGCTGCCGTTGGCCGAGTGC 1417
        |||||
Qy      109 CysGluArgAlaLysAlaGlyCysSerProLeuMetArgGlnTYrGlyPheAlaTrpPro 128
        |||||
Db      1418 TCGGAGAGAGCCCGCTGGATGCGACCCATCATGACGATGACGTTGCAATGGCCG 1477
        |||||
Qy      129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet 148
        |||||
Db      1478 GAGAGAAATGGCGTGGAGCACTTCTCTTCATGGT---GACCCGACAATCTGTGATG 1534
        |||||
Qy      149 AspTYr----- 150
        |||||
Db      1535 GAACAGCCCTGCTACACGAGAGCTGGCAGCGGTGGACGCTGGCGGATCGGGTGGCTCT 1594
        |||||
Qy      150 ----- 150
        |||||
Db      1595 GGCACGCGTTCCGGCTCGCGGGCAACGGAAGCAGCAGTGGCTCGGCGCGCACT 1654
        |||||
Qy      151 -----AsnArgSerGluAlaThrThraLapProArgProPheProAlaLys 166
        |||||
Db      1655 GGGCGCGGCGGACAGCGGTTCCACCTCAACGAAAGCCGTGCGCGGACGCAATTCAAA 1714
        |||||
Qy      167 ProThrLeuProGlyProGlyAlaProAlaSerGlyGlyGluCysProAlaGly 186
        |||||
Db      1715 --AATGCCAAMATCCCAAGAGAAAGCAAGCGGAAAGAGTGCAGC----- 1762
        |||||
Qy      187 ProPheValCysLysCysArgGluProPheVal----- 197
        |||||
Db      1763 -----TCTGTGCGCGCTCCCACTCATCTTCTCGGGAGAGACAGCTGCTGCAG 1813
        |||||
Qy      198 -----ProIleLeuLysGluSerHisProLeuTYrAsnLysVal----- 210
        |||||
Db      1814 CAGCAGTCGAGATGCCATGATGACATCATCACACCACTGATCATGACCTCATCTGTC 1873
        |||||
Qy      211 ---ArgThrGlyGlnValProAsnCysAlaValProCysTYrGlnProSerPheSerAla 229
        |||||
Db      1874 CAAAGGATCGCGCGCTTCCAAACTGCGCATACCGTCAAGGGGCCCTTCTTCAGCAAC 1933
        |||||
Qy      230 AepgluArgThrPheAla 235
        |||||
Db      1934 GACGAAAGGATTTGCC 1951

RESULT 8
ID      AAT89891 standard; DNA; 2259 BP.
XX      AAT89891;
AC      AAT89891;
DT      27-APR-1998 (first entry)
DE      Mouse frizzled gene 7 (Mfz7) encoding a Wnt receptor.
XX      Wnt receptor; mouse frizzled gene 7; Mfz7 gene;
KW      signal transduction; cancer; cell growth; cell proliferation;
KW      mammary tumour; oncogene; therapy; ds.
XX      Mus musculus.
OS      Mus musculus.
FH      Key Location/Qualifiers
FT      CDS 361..2079
FT      /*tag= a

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XX Claim 3; Page 192-193; 410pp; English.
 CC Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is the coding sequence
 CC for a human protein which has at least one hydrophobic domain. The
 CC protein encoded by the present sequence may be a secretory or a membrane
 CC protein. The encoded protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity, haemostatic
 CC and thrombolytic activity, anti-inflammatory activity and tumour
 CC inhibition activity. The present sequence could therefore be used for
 CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
 CC disease, and cancer via gene therapy.

SQ Sequence 1941 BP; 317 A; 642 C; 629 G; 353 T; 0 other;

Alignment Scores:

Pred. No.:	1,64e-20	Length:	1941
Score:	415.00	Matches:	104
Percent Similarity:	46.37%	Conservative:	30
Best Local Similarity:	35.99%	Mismatches:	87
Query Match:	31.68%	Indels:	68
DB:	21	Gaps:	11

US-09-847-102a-68 (1-235) x AAA60179 (1-1941)

QY 3 ArgPro-----AspProSerAlaProProSerLeuLeuLeuLeu----- 17
 DB 127 GCGCCGCCAGTTGATCCCGCGGATGGCGCCGCAAGCTCTCTGCTGTTGGCTGCTG 186
 QY 18 -----AlaGlnLeuValGly---ArgAlaAlaAlaSerLeuAlaPro----- 31
 DB 187 GAGGCTCCGCTCTGCTGGGGGTCCGAGGCCGCGGCGGCGGCGGCGGCGGCGGCGG 246
 QY 31 ----- 31
 DB 247 CCGGGGCGGGGCGAGCAACCGCGCGCGCTCAGCAGCAACAGCGGGGCGAGCTAC 306
 QY 32 -----ValGlyGlnGlnIleThrValPro 39
 DB 307 AACGGCGAGCGGGGATCTCCCTCCGCGACACAGGCTATTGGCCATCTCCATCCCG 366
 QY 40 MetCysArgGlyIleGlyThrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThr 59
 DB 367 CTGTGACGAGACATGCGGTAAACAGACCATCATGCCCCAACCCTGCTGGGCCACAGAAC 426
 QY 60 GlnAspGlnAlaGlyLeuGlnValHisGlnPheTrpProLeuValGlnIleCysSer 79
 DB 427 CAGGAGGAGCGGGGCTGGAGGTGACACGAGTCTACCCCTCTGTAAGTGCAGTGTTC 486
 QY 80 ProAspLeuArgPhePheLeuCysThrMetIleThrProIleCysLeuProAspTrpHis 99
 DB 487 GCTGAGCTCAAGTCTCTCTGCTGCTCATGTACGCGCCCTGTGCACCGCTG---CTAGAG 543
 QY 100 LysProLeuProProCysArgSerValCysGlnArgAlaValAlaGlyCysSerProLeu 119
 DB 544 CAGGGCGTGGCCCGCTCCGCTCCCTGTGCGAGCGGCGCGGCGGCGGCGGCGGCGGCTC 603
 QY 120 MetArgGlnIleValPheAlaTrpProGlnArgMetSerCysAspArgLeuProValLeu 139
 DB 604 ATGAACAAGTTCGGGCTTCAGTGGCGGCGACAGCGCTCAAGTGTGAGAGTTCGCGGCGAC 663
 QY 140 GlyArgAspAlaGlnValLeuCysMetAspTrpAsnArgSerGlnAlaThrThrAlaPro 159
 DB 664 GGC-----GCCGCGAGCTGTGCGTGGCGCCAGAACCTCCGACAGGCGGCCGACG 717
 QY 160 ProArgProPheProAlaLysProThrLysProGlyProProGlyValAlaProLysArg 179
 DB 718 CCTGCTGCTCTCCAGAGTTCGAGACGACCAACCTCAGACGCGGCGGAGGCGACCGCT 777

QY 180 GlyIleCysProAlaGly-----GlyProPheValCysLeuCysArg 193
 DB 778 GCGGCTCTCCGGGGGGCGCGCGCTGAGAGCGAGCAAGTTCCTGCGCCG---GCG 834
 QY 194 GlnProPheValProIleLeuLysGlnSerHisProLeuIleValValArgThrGly 213
 DB 835 GCCCTCAAGGTGCGCTCTTACTCACTCACTCACTCTGCGGAGAGG----- 882
 QY 214 GlnValProAsnCysAlaValAlaProCysTrpGlnProSer----- 226
 DB 883 -----GACTGGGGGCGACCTTGT---GAGCCGACCAAGTGTATGGCTCATGTAC 930
 QY 227 PheSerAlaAspGlnArgThrPheAla 235
 DB 931 TTCGGCGCCGAGAGACTCGCTTCTCG 957
 RESULT 10
 AAA60189
 ID AAA60189 standard; DNA; 4485 BP.
 XX
 AC AAA60189;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Hydrophobic domain protein cDNA HP02539 isolated from Saos-2 cells.
 XX
 KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;
 KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
 KW gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20029448-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 17-NOV-1999; 99WO-JP06412.
 XX
 PR 17-NOV-1998; 98JP-0326255.
 XX
 PR 22-DEC-1998; 98JP-0364315.
 XX
 PR 16-MAR-1999; 99JP-0069811.
 XX
 PR 27-APR-1999; 98JP-0192299.
 XX
 PR 19-MAY-1999; 99JP-0138169.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 PI Kato S, Kimura T;
 XX
 DR WPI; 2000-387753/33.
 DR P-PSDB; AAB12117.
 XX
 PT Proteins comprising hydrophobic regions, such as secretory and membrane
 PT proteins, useful in research and diagnostics and having various
 PT activities e.g. immunomodulatory, anti-inflammatory, chemokinetic,
 PT hemostatic, thrombolytic.
 XX
 PS Claim 4; Page 199-204; 410pp; English.
 CC Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is the coding sequence
 CC for a human protein which has at least one hydrophobic domain. The
 CC protein encoded by the present sequence may be a secretory or a membrane
 CC protein. The encoded protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, anti-inflammatory activity and tumour
inhibition activity. The present sequence could therefore be used for
treatment of autoimmune disease, Alzheimer's disease, Parkinson's
disease, and cancer via gene therapy.

XX Sequence 4485 BP; 1002 A; 1198 C; 1193 G; 1092 T; 0 other;

Alignment Scores:

Pred. No.:	4.17e-20	Length:	4485
Score:	415.00	Matches:	104
Percent Similarity:	46.37%	Conservative:	30
Best Local Similarity:	35.99%	Mismatches:	87
Query Match:	31.68%	Indels:	68
DB:	21	Gaps:	11

US-09-847-102a-68 (1-235) x AAA60189 (1-4485)

```

QY 3 ArgPro-----AspProSerAlaProProSerLeuLeuLeuLeuLeu----- 17
   |||||
DB 315 CCGCCCGCAGATTGACCCCGCGCGATTGGCGCGCCACCTGCTGCTGCTTGGCTGCTG 374
   |||||
QY 18 -----AlaGlnLeuValGly--ArgAlaAlaAlaAlaSerLysAlaPro----- 31
   |||||
DB 375 GAGGCTCCGCTGCTGCTGGGGGCTCCGGGCCAGCGCGCGCCAGGGCCAGGCCAGGGG 434
   |||||
QY 31 ----- 31
   |||||
DB 435 CCGCGCGCGCGCGAGCAGCAGCCCGCGCGCTCAGCAGCAGCAGCGCGCGCAGTAC 494
   |||||
QY 32 -----ValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 39
   |||||
DB 495 AACGGCGAGCGGGGAGCTCCCGTCCCGGACACAGCGGATTATGCGCGCCATCTCCACCCG 554
   |||||
QY 40 MetCysArgGlyYllGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThr 59
   |||||
DB 555 CTGTGACGAGCATTCGCGTCAACACGACCATATGCTCCACCTGCTGGGCCACAGAAC 614
   |||||
QY 60 GlnAspGlnAlaGlyLeuGlnValHisGlnPheThrProLeuValGlnLeuGlnCysSer 79
   |||||
DB 615 CAGAGAGACGCGCGCGCTGAGGAGGACCACTTCTACCTCTAGTGAAGAGCAGTCTTC 674
   |||||
QY 80 ProAspLeuArgPhePheLeuLeuCysThrMetTyrThrProLecCysLeuProAspTyrHis 99
   |||||
DB 675 GCTGACTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731
   |||||
QY 100 LysProLeuProProCysArgSerValCysGlnArgAlaLysAlaGlyCysSerProLeu 119
   |||||
DB 732 CAGGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
   |||||
QY 120 MetArgGlnTyrGlyPheAlaTyrProGlnArgMetSerCysAspArgLeuProValLeu 139
   |||||
DB 792 ATGAACAGATTGCGGCTTCCAGTGGCCAGACAGCTCAAGTGTAGAAGTTCGCGGTGCAC 851
   |||||
QY 140 GlyArgAspAlaGlnValLeuLeuCysMetAspTyrAsnArgSerGlnAlaThrThrAlaPro 159
   |||||
DB 852 GGC-----GCCGGCAGAGCTGTGCGGGCCAGACAGCTCCAGCAAGGACCCCGACAG 905
   |||||
QY 160 ProArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 179
   |||||
DB 906 CCTCGCTGCTTCCAGAGTTCGTGACACGACACCTCAGACAGCGCGCGGAGGACCGCT 965
   |||||
QY 180 GlnGlnCysProAlaGly-----GlyProPheValCysLysCysArg 193
   |||||
DB 966 GGGGGCTTCCCGGGGGCGCGCGCGCGCTGCGAGCGAGGAGGAGTTCCTCCGCGCG---CCG 1022
   |||||
QY 194 GlnProPheValProLeuLeuLysGlnSerHisProLeuTyrAsnLysValArgThrGly 213
   |||||
DB 1023 GCCCTCAAGTGCCTTCACTCACTCACTCACTCACTTCTTGGGAGAG----- 1070
   |||||
QY 214 GlnValProAsnGlnAlaValProCysTyrGlnProSer----- 226
   |||||
DB 1071 -----GACTGCGGGCGCAGCTTGT---GAGCCGACCAAGGTGTATGGGCTCATGTAC 1118
   |||||

```

QY 227 PheSerAlaAspGlnArgThrPheAla 235
DB 1119 TTCGGGCCGAGAGAGCTGCGCTTCTCG 1145

RESULT 11

ID ABK63777 standard, cDNA, 4540 BP.

ABK63777;

18-JUN-2002 (first entry)

Rat sequence differentially expressed in response to a hepatotoxin #1684.

Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;

KW differential expression; centrilobular necrosis; steatosis.

OS Rattus norvegicus.

PN WO200210453-A2.

PD 07-FEB-2002.

PF 30-JUL-2001; 2001WO-US23872.

PR 31-JUL-2000; 2000US-222040P.

PR 02-NOV-2000; 2000US-244880P.

PR 11-MAY-2001; 2001US-290029P.

PR 15-MAY-2001; 2001US-290645P.

PR 22-MAY-2001; 2001US-292336P.

PR 06-JUN-2001; 2001US-295798P.

PR 13-JUN-2001; 2001US-297457P.

PR 19-JUN-2001; 2001US-298884P.

PR 09-JUL-2001; 2001US-303459P.

PA (GENE-) GENE LOGIC INC.

PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

DR WPI; 2002-241625/29.

XX Predicting toxic effects of compounds or the progression of these toxic

PT effects by determining the changes in gene expression in tissues or

PT cells exposed to the toxin and comparing these to gene expression in

PT unexposed tissues or cells.

PS Claim 1; Seq ID No 1684; 239pp; English.

XX The invention relates to methods for predicting toxic effects of

CC compounds or the progression of these toxic effects by determining the

CC global changes in gene expression in tissues or cells exposed to the

CC toxin and comparing these to gene expression in unexposed tissues or

CC cells. Also included are methods of predicting at least one toxic

CC effect of a compound or progression of a toxic effect, preferably the

CC hepatotoxicity of a compound, comprising detecting the level of

CC expression in a tissue or cell sample exposed to the compound of two or

CC more genes listed in the specification, where differential expression of

CC the genes is indicative of at least one toxic effect or progression.

CC The method can also be used to identify an agent which modulates the

CC toxic response and predict cellular pathways that a compound modulates

CC in a cell. The methods utilize a set of at least two probes (on a solid

CC support in kit form), where each of the probes comprises a sequence that

CC specifically hybridizes to a gene listed in the specification, a computer

CC system comprising a database containing information identifying the

CC expression level in a tissue or cell sample exposed to a hepatotoxin of a

CC set of genes comprising at least two genes listed in the specification,

CC and a user interface to view the information used to present information

CC identifying the expression level in a tissue or cell of at least one gene

CC listed in the specification. The method is useful for elucidating global

CC changes in gene expression and for identifying toxicity markers in

CC tissues or cell exposed to a known toxin. The genes may be used as

CC toxicity markers in drug screening and toxicity assays. The genes and

CC gene expression information may be used as diagnostic markers for the

CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterized by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.

XX SQ Sequence 4540 BP, 998 A, 1255 C, 1220 G, 1067 T, 0 other;

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Best Local Similarity:	Mismatches:	Indels:	Gaps:
6, 8e-19	4540	398.00	88	28	40.74%	26	8	
Percent Similarity:		53.70%						
Query Match:		30.38%						

US-09-847-102a-68 (1-235) x ABE63777 (1-4540)

33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 1096 TGTCAAGCCATCTCCATCCCGGTGTGACGACATGCGTAAATCAGACATCATGCCCC 1155
 53 AanglnPhaAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72
 1156 AACCTGCTGGCCACACGAAATCAGAGACGCGCGCTGAGGTGACACAGTTCTAACCCG 1215
 73 LeuValGluIleGlnCysSerProAspLeuArgPheLeuGlnCysThrMetTyrThrPro 92
 1216 TTGCTCAAGGTGACGCTGCTCAGCCAGCTCAAGTTCTTCTGTGCTCCTGACGCGCTT 1275
 93 IleCysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluArgAla 112
 1276 GTGTGACCGGTA---CTGAGACGAGCGCTGCTCCTGCGCGCTCCTGCGGAGCGCGCC 1332
 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132
 1333 CAG---GGCTGGCAGGCACTCATGAACAGTTCCGCTTCAGGCGCACACGCTCAAG 1389
 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuGlnCysMetAspTyrAsnArg 152
 1390 TCCGAGAAATTCCTCTGTGACAGCG---GCAAGAGAGCTGTGCTGCGGCGCAGAACACT 1443
 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
 1444 TCCGACAAAGCACCAGCCGACCTCCTGCTGCGGAGTTGAGCAGCAGATCCGAG 1503
 173 ProGlyAlaProAlaSerIleGlyLysProAlaGly-----Gly 186
 1504 CACGGGGGGGTGTACCGCGCGGCTACCGGGAGGAGTCCGCGCCGCTGAGCGGGGA 1563
 187 ProPheValCysIleCysArgGluProPheValProIleLeuLysGlnSerHisProLeu 206
 1564 AAGTTCTCTGCGCG---CGCGCCCTCAGAGGTGCTTCTTCTACTCACTATCATCTTTG 1620
 207 TyrAsnLysValArgThrGlnGlnValProAsnCysAlaValAlaProCysTyrGlnProSer 226
 1621 GGGGAGAAAG-----GACTGCGGGCGCGCTGCG---GAACTCACT 1656
 227 -----PheSerAlaAspGluArgThrPheAla 235
 1657 AAAGTATACGGGCTCATGTACTTGGCGCTGAGAGTTCGCTTTTCG. 1704

Db 1657 AAAGTATACGGGCTCATGTACTTGGCGCTGAGAGTTCGCTTTTCG. 1704

RESULT 12
 AAF75974
 ID AAF75974 standard; cDNA, 3269 BP.
 XX AAF75974;
 AC AAF75974;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human frizzled family gene 584 cDNA.
 XX
 KW Human; frizzled family gene 584; embryo; foetus; cancer;

KW drug discovery; cytostatic; ss.

XX Homo sapiens.

XX WO200112808-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-JP05552.

XX 18-AUG-1999; 99JP-0232018.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Senoo C, Numata M;

XX WPI, 2001-211220/21.

XX P-PSDB; AAB37708.

PT Novel frizzled family genes 584 strongly expressed in embryo and fetus
 as well as in cancer cells, useful in drug development for diseases
 with abnormal expression including tumor

PS Claim 1; Fig 6-7; 89pp; Japanese.

CC The invention relates to a novel frizzled family gene, 584, from mouse
 and human (cDNAs given in AAF75973 and AAF75974), and to the mouse and
 human 584 proteins (AAB73307, AAB73308). Gene 584 is strongly expressed
 in the embryo and foetus, and is also strongly expressed in cancer
 cells. The invention also relates to recombinant vectors and host
 cells comprising gene 584 nucleic acids, the recombinant expression of
 the 584 protein, methods of screening for modulators of 584 activity or
 CC expression, and the compounds thus identified. The human and mouse 584
 CC genes represent a novel gene target for the development of drugs useful
 in the treatment of diseases such as cancer. The present sequence
 CC represents human gene 584 cDNA.

SQ Sequence 3269 BP, 688 A, 961 C, 941 G, 668 T, 11 other;

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Best Local Similarity:	Mismatches:	Indels:	Gaps:
2, 84e-18	3269	387.00	88	28	50.88%	71	42	
Percent Similarity:		50.88%						
Query Match:		29.54%						

US-09-847-102a-68 (1-235) x AAF75974 (1-3269)

1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
 486 ATGCAAGCCCGCGGCGCCCGC-----CTGTGCTGTGCTCTGACAGTG 527
 21 ValGlyArgAlaAlaAlaAlaSerIleValAlaProVal-----Cys 33
 528 ATGGCTGCTGGCGCGCATCATGACATGAGCGCGCGGCGCAGCAATGTC 587
 34 GlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetProAn 53
 588 CAGCCCATCGAATCCGATGCAAGACATCGGCTCAACATGACTGTGTGCGCAAC 647
 54 GlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeu 73
 648 CTGATGGGCGCAGAACACGAGCGAGCGACATCCAGTTCACAGAGTTCGCGCGCTG 707
 74 ValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrProIle 93
 708 GTGAGTACGCTGCGCAGCGCACTCCGCTTCTTCTGTGCTGCTGACGCGCGATG 767
 94 CysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluArgAlaLys 113
 768 TGCACCGAGCAGAGTCTTACCCCATCCCGCGGTGCTGATGTGAGAGGCGCGG 827

PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX (AVAL-) AVALION PHARM.
 XX
 PA
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 DX MPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX
 PS Claim 1; SEQ ID 282; 44pp: English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL1664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytosolic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 1909 BP; 523 A; 441 C; 437 G; 507 T; 1 other;

Alignment Scores:
 Pred. No.: 4.51e-18 Length: 1909
 Score: 380.50 Matches: 83
 Percent Similarity: 50.00% Conservative: 83
 Best Local Similarity: 35.17% Mismatches: 83
 Query Match: 29.05% Indels: 35
 DB: 24 Gaps: 8

US-09-847-102a-68 (1-235) x ABL61945 (1-1909)

OY 4 ProAspProSer-----AlaProSerLeuLeuLeuLeuAla 18
 DB 52 CCCATCTCTGCGGATCATGTCTGCGGAGCCCGGAGGAGGAGTCTGCTGCGGACC 111

OY 19 GlnLeuValGlyArgAlaAala-----AlaAlaSerLeuAlaProVal 32
 DB 112 GGGCTGCTTGCCCTGCTGCTCTGCTGCTCCGGGTGCCCCGGGCTCGGCTCAGACC 171
 OY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 DB 172 TGTGAGCCCGTCGCATCCCTGTGCAAGTCCCTGCGCCCTGGAGACATGATGATGCC 231
 OY 53 AsnGlnPheAsnHisAspThrGlnAspGluIleGlyLeuGluValHisGlnPheThrPro 72
 DB 232 AACCACTGCACACACAGACTCAGAGCAACGCCATCTGCGCATGAGAGATTCCAGAGT 291
 OY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrTyrThrPro 92
 DB 292 CTGCTGGGACCACTGACAGCCCGCATCTGCTCTCTCTGTCGACATGACCGGCC 351
 OY 93 IleCysLeuProAspTyr---HisIysProLeuProProCysArgSerValCysGluArg 111
 DB 352 ATCTGACCATTCATGCTTCAGACAGCCCATCAAGCCCTGTAACTGTGTGCGACGG 411
 OY 112 AlaIysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMet 131
 DB 412 GCCCGCAGGCGCTGTGAGCCCATCTACTCATCAAGTACCGCACTGCGCGGAGAACCTG 471
 OY 132 SerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMetAspTyrAsn 151
 DB 472 GCCTCGAGGAGACTCCAGTGTACGACAGAGGGCC-----GTGTGATC-----TCT 516
 OY 152 ArgSerGluAlaThrThrAlaProProArgProPheProAlaIysProThrLeuProGly 171
 DB 517 CCCGAGGCCATCGTTACTGCGGAGCGAGCTGATTTTCT----- 555
 OY 172 ProProGlyAlaProAlaSerGlyGlyCysProAlaGlyGlyProPheValCysIys 191
 DB 556 -----ATGCAATTCTAGTAAGGAAGTCTAGAGGGGCAAGAGTGAACCTGTAA 606
 OY 192 CysArgGluProPheValProIleuIysGlnSerHisProLeu-----Tyr 207
 DB 607 TGTAA-----CTATTAGCTACACAGAACCTATTTCGGAAACATTAAC 654
 OY 208 AsnIysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
 DB 655 AACATATGATTCGGGCTTAAGTTAAAGAGATAAAGACTAACTGATTCAT 702

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Title: US-09-847-102A-68

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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	378	28.9	1893	3	US-08-878-474-10 Sequence 10, Appl
2	372.5	28.4	2039	3	US-09-276-531-45 Sequence 45, Appl
3	367	28.0	2176	3	US-08-878-474-8 Sequence 8, Appl
4	360	27.5	1875	3	US-08-878-474-4 Sequence 4, Appl
5	342.5	26.1	2009	4	US-09-276-531-108 Sequence 108, App
6	297	22.7	1796	4	US-09-276-531-113 Sequence 113, App
7	284.5	21.7	1796	4	US-08-937-067-1 Sequence 1, Appl
8	282	21.5	2833	4	US-09-276-531-23 Sequence 23, Appl
9	280	21.5	2880	2	US-08-987-289-1 Sequence 1, Appl
10	274.5	21.0	1984	4	US-08-937-067-5 Sequence 5, Appl
11	271	20.7	870	4	US-08-937-067-3 Sequence 3, Appl
12	246	18.8	1146	4	US-08-893-654B-5 Sequence 5, Appl

13	240.5	18.4	1308	4	US-08-937-067-18 Sequence 18, Appl
14	240.5	18.4	4245	4	US-09-276-531-16 Sequence 16, Appl
15	231.5	17.7	2190	4	US-08-893-654B-1 Sequence 1, Appl
16	231	17.6	1140	4	US-08-893-654B-3 Sequence 3, Appl
17	227.5	17.4	502	4	US-08-893-654B-7 Sequence 7, Appl
18	142	10.8	1739	2	US-08-681-151-2 Sequence 2, Appl
19	139.5	10.6	2972	2	US-08-720-484A-3 Sequence 3, Appl
20	139.5	10.6	2972	2	US-08-953-823A-3 Sequence 3, Appl
21	139.5	10.6	2972	2	US-08-953-823A-3 Sequence 3, Appl
22	130	9.9	3854	2	US-08-720-484A-1 Sequence 1, Appl
23	130	9.9	3854	2	US-08-953-823A-1 Sequence 1, Appl
24	130	9.9	3854	2	US-08-953-823A-1 Sequence 1, Appl
25	118	9.0	34063	4	US-09-453-702B-96 Sequence 96, Appl
26	112.5	8.6	53526	3	US-08-658-136-2 Sequence 2, Appl
27	112.5	8.6	53526	3	US-08-658-136-1 Sequence 1, Appl
28	111	8.5	4220	4	US-08-765-907A-14 Sequence 14, Appl
29	110.5	8.4	4496	4	US-08-765-907A-6 Sequence 6, Appl
30	107.5	8.2	2604	5	PCT-US95-08493-20 Sequence 20, Appl
31	107	8.2	3901	1	US-08-188-562-31 Sequence 31, Appl
32	107	8.2	3901	1	US-08-646-715-31 Sequence 31, Appl
33	106	8.1	36919	3	US-08-923-137-2 Sequence 2, Appl
34	105.5	8.1	3879	4	US-08-916-352-1 Sequence 1, Appl
35	105.5	8.1	5836	4	US-09-453-702B-253 Sequence 253, App
36	105.5	8.1	4403765	4	US-09-103-840A-2 Sequence 2, Appl
37	105.5	8.1	4411529	4	US-09-103-840A-1 Sequence 1, Appl
38	105	8.0	1265	1	US-08-132-649-5 Sequence 5, Appl
39	105	8.0	1265	3	US-08-767-579-5 Sequence 5, Appl
40	105	8.0	2430	4	US-09-233-160-16 Sequence 16, Appl
41	103.5	7.9	48908	4	US-09-453-702B-137 Sequence 137, App
42	103	7.9	3777	3	US-09-121-321-15 Sequence 15, Appl
43	103	7.9	3777	4	US-08-933-803A-15 Sequence 15, Appl
44	103	7.9	4403765	4	US-09-103-840A-2 Sequence 2, Appl
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ALIGNMENTS

RESULT 1
US-08-878-474-10
Sequence 10, Application US/08878474
Patent No. 6133232
GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
APPLICANT: Boumeester, Lewis
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878, 474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418

QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThreTyrThrPro 92
 DB 430 CTGCTGGGACCCACCCAGCCGATCTGCTCTTCTCTGCGCATGTACCGCGCC 489
 QY 93 IleCysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGluArg 111
 DB 490 ATCTCACCATTGACTTCCAGACACAGCCCATCAAGCCCTGTAGAGTGTGTGCGAGCGG 549
 QY 112 AlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGluArgMet 131
 DB 550 GCCCGGACAGGCTGTGAGCCCATCTCATCAAGTACCCGACATCGTGGCGGAGAACTGG 609
 QY 132 SerCysAspArgLysLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsn 151
 DB 610 GCCTCGAGAGACTCCAGTGTACGACAGGGGCGC-----GTGTGCATC-----TCT 654
 QY 152 ArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGly 171
 DB 655 CCCGAGGCCATCTTACTGCGGACGAGCTGATTTTCT----- 693
 QY 172 ProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyProPheValCysLys 191
 DB 694 -----ATGGATTCTTAGTAAGGAAACTGTAGAGGGCGCAAGAGTAAAGCTGTAA 744
 QY 192 CysAlaGluProPheValProIleLeuLysGlySerHisProLeu-----Tyr 207
 DB 745 TGTAG-----CTATTAGAGCTACACAGAACCTATTTCGGAACAATTAC 792
 QY 208 AsnLysValArgThrGlyGlnValProAsnGlyAlaValProCysTyr 223
 DB 793 AACTATGCTATTCGGGCTAAAGTAAAGATTAAGACTAAGTGGCAT 840
 RESULT 3
 US-08-878-474-8
 ; Sequence 8, Application US/08878474
 ; Patent No. 6133232
 ; GENERAL INFORMATION:
 ; APPLICANT: De Robertis, Edward M.
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; TITLE OF INVENTION: Factors
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Majestic, Parsons, Siebert & Haue
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 94111-4106
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/878,474
 ; FILING DATE: 18-JUN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/020,150
 ; FILING DATE: 20-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Siebert, J. Suzanne
 ; REGISTRATION NUMBER: 28,758
 ; REFERENCE/DOCKET NUMBER: 3100.002US1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/248-5500
 ; TELEFAX: 415/362-5418
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2176 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double

; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-878-474-8
 Alignment Scores:
 Pred. No.: 3,956-22 Length: 2176
 Score: 367.00 Matches: 77
 Percent Similarity: 51.63% Conservative: 34
 Best Local Similarity: 35.81% Mismatches: 80
 Query Match: 28.02% Indels: 24
 DB: 3 Gaps: 6

US-09-847-102a-68 (1-235) x US-08-878-474-8 (1-2176)

QY 14 LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaSerLysAlaProValCys 33
 DB 58 TTGCTAGTCTGTGGCTGCTCTCTGCTGCTCCAGTCCCGGAGCTCAGGCTCCACCTGT 117
 QY 34 GlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetProAsn 53
 DB 118 GAGCTGTCCCATCTCCCTGTGCAAGTCCCTTCCCTGGAACATGACCAAGATGCCCAAC 177
 QY 54 GlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheThrProLeu 73
 DB 178 CACTGCACACACAGCACCCAGCTTAACCCATCTGCGCCATGGAACAGTTGCAAGGCTG 237
 QY 74 ValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThreTyrThrProIle 93
 DB 238 CTGGCCACCCACTGTAGAGCCCGGATCTTCTTCTCTCTGTGCAATGATGACACCAT 297
 QY 94 CysLeuProAspTyr--HisLysProLeuProProCysArgSerValCysGluArgAla 112
 DB 298 TGCAACATGACTTCACACACAGAGCCCATCAAGCCCTCAAGTGTGTGTAGCGCGCC 357
 QY 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGluArgMetSer 132
 DB 358 CGACAGGGCTCGAGCCCATCTCATCAAGTAAAGCCGCACTGTGGCCGAAAGCTTGCC 417
 QY 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
 DB 418 TCGCAGCAGCTGCCGCTGTAGACCGCGC-----GTGTGCATC-----TCTCT 462
 QY 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
 DB 463 GAGGCCATGTCACCGCGGACGAGCGGATTTTCT----- 498
 QY 173 ProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyProPheValCysLysCys 192
 DB 499 -----ATGATTCAAGTACTGACACTGACAGAGGGGCAAGCAGCAAGCTTGCAAAATGT 552
 QY 193 ArgGluProPheValProIleLeuLysGlySerHisProLeu-----TyrAsn 208
 DB 553 AAG-----CTGTGAGAGCTACACAGAAAGCTATTTCGGAACAATTACAAAC 600
 QY 209 LysValArgThrGlyGlnValProAsnGlyAlaValProCysTyr 223
 DB 601 TATGTCATCGGCGCTAAAGTTAAAGAGTAAAGATGAATGATCAT 645
 RESULT 4
 US-08-878-474-4
 ; Sequence 4, Application US/08878474
 ; Patent No. 6133232
 ; GENERAL INFORMATION:
 ; APPLICANT: De Robertis, Edward M.
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; TITLE OF INVENTION: Factors
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Majestic, Parsons, Siebert & Haue
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California

COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002051
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418
INFORMATION FOR SEQ. ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1875 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-878-474-4

Alignment Scores:
Pred. No.: 1,276-21 Length: 1875
Score: 360.00 Matches: 83
Percent Similarity: 52.23% Conservative: 34
Best Local Similarity: 37.05% Mismatches: 73
Query Match: 27,488 Indels: 34
Gaps: 10

US-09-847-102a-68 (1-235) x US-08-878-474-4 (1-1875)

8 AlaProProSerLeuLeuLeuLeuLeuValGlyArgAlaAlaAla 27
366 GCCATACCTGAGCTGGCGCTTCTTATTATCC-----AATGCTTACTGTGT 413
28 SerLysAlaProValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsn 47
414 TCG-----TGTAGCCTGTGCGGATCCCATGTGCAAACTATGATGCATGGAAC 461
48 LeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGlnValGlyLeuGlnVal 67
462 ATGACCAAGATGCCCAACCATCTCCACACAGACATCAAGCCAAATGCTGCGCAATT 521
68 HisGlnPheThrProLeuValGlnIleGlnCysSerProAsnLeuArgPhePheLeuCys 87
522 GAACAGTTTGAAGTTTGCTGACCACTGATGAGCCAGACCTTTGTTCTTCTGTGT 581
88 ThrMetTyrThrProIleCysLeuProAspTyr---HisLysProLeuProProCysArg 106
582 GCCATGTATGCCCCCTTTGTACCATGATTTCCACATGACATGACATTAAGCTTCAAG 641
107 SerValCysGlnArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAla 126
642 TCCGTGTGGAAGAGGCGCCAGCGGCTGTGAGCCCATTTCTATAAGTATACCGCACACT 701
127 TyrProGlnArgMetSerCysAspArgLeuProValLeuGlnValArgAspAlaGlnValLeu 146
702 TGGCCAGAGAGCTGCGCATGTGAAGAGCTGCCGTATATGACAGAGA-----GTC 752
147 CysMetAspTyrAsnArgSerGlnAlaThrThrAlaProProArgProPheProAlaLys 166
753 TGCATCTCC-----CCAGAGGCTATCGTACACGTGGAACAGAAACAGATTAAAG 803
167 ProThrLeuProGlnProProGlnAlaProAlaSerGlyGlyGlnCysProAlaGlyGly 186

804 CCAGACTTC-----TCCATGATTCAAAACAATGAAATTCGGAAGCGGCAG 851
187 ProPheValCysLysCysArgGlnProPheValProIle----- 199
852 GAGCAC---TGTAAATGCAAG-----CCATGAAGGCAACCCAAAGACTTAT 896
200 LeuLysGlnSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAla 219
897 CTCAGAAATTAAT-----TACAATTATGTAATCAGAGCAAAAGTGAAGAGTGAAA 947
220 ValProCysTyr 223
948 GTGAATGCCAC 959

RESULT 5

US-09-276-531-108
Sequence 108, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Reddy, Roopa

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murry, Ph.D.

REGISTRATION NUMBER: 42,918

REFERENCE/DOCKET NUMBER: PA-0008 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ. ID NO.: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 2009 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BRSTNOT07

CLONE: 212411

US-09-276-531-108

Alignment Scores:

Pred. No.:	4,186-20	Length:	2009
Score:	342.50	Matches:	74
Percent Similarity:	50.68%	Conservative:	37
Best Local Similarity:	33.79%	Mismatches:	83

TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2833 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: FIBRANT01
 CLONE: 150629
 US-09-276-531-23

Alignment Scores:

Pred. No.:	8.33e-15	Length:	2833
Score:	282.00	Matches:	65
Percent Similarity:	41.23%	Conservative:	80
Best Local Similarity:	30.81%	Mismatches:	22
Query Match:	21.53%	Indels:	44
DB:	4	Gaps:	6

US-09-847-102a-68 (1-235) x US-09-276-531-23 (1-2833)

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QY 33 CysGlnGluIleThValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 TGTGAACCAATTAATCTGTTCCAGATGTATGAAATGGCTTACACATGACGTTTTCCT 300

QY 53 AenglnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheThrPro 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 AATCTGATGGCTATTATATACCAAGACTATTTGCCGCGGTGAAATGAGCATTTTCTCT 360

QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThrPro 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 CTCGCAAACTCGAATGTTTACCAAAACATTGAACTTTCTCTCGCAAAACATTGTTGACA 420

QY 93 IleCysLeuProAspTyrHisIleAspLeuProProCysArgSerValCysGluArgAla 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 ACCTGATGAAACAAATTCAT---GTGGTTCACCTTGTCTGTTAACTTTGTGAGAAAGTA 477

QY 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaThrProGluArgMetSer 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 478 TATTTGATGCAAAAAATTAATATGACACTTTGGATGCCATGGCTGAGAGCTTGAA 537

QY 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 538 TGTGACAGTTTACATACCTGTGATGAGACTGTTCCTGTA----- 576

QY 153 SerGluAlaThrThrAlaProProArgProPhe-----ProAlaLysProThrLeuPro 170
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 577 -----ACTTTGATCCACACACAGAAATTTCTTGTCTGTCGGAAGAAACA----- 621

QY 171 GlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyLysProPheValCys 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 622 -----GACCAATGTCMAAGACATTGCAATTTGGTGT 654

QY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeuTyrAsnLysVal 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 -----CCAAAGCATTTTAAAGACT 672

QY 211 ArgThrGlyGln-----ValProAsnCysAlaValProCysTyrGln 224
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 673 TCTGGGGGCAAGATATAGTTTCTGGGAATTGACAGTGTGCGCTCCATGCCCAAC 732

QY 225 ProSerPheSerAlaAspGluArgThrPheAla 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 733 ATGTATTTTAAAGTATGAGCTAGAGTTTGCA 765
  
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RESULT 9

US-08-987-289-1
 Sequence 1, Application US/08987289
 Patent No. 5994098
 GENERAL INFORMATION:
 APPLICANT: HU, ERDING

APPLICANT: ZHU, YUAN
 TITLE OF INVENTION: A Human 7-TM Receptor Similar
 TITLE OF INVENTION: to Murine Fizzled-6 gene
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RATNER & PRESTIA
 STREET: P.O. BOX 980
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/987,289
 FILING DATE: 09-DEC-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/048,725
 FILING DATE: 02-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-70060
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701

TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2880 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

US-08-987-289-1

Pred. No.:	8.51e-15	Length:	2880
Score:	282.00	Matches:	65
Percent Similarity:	41.23%	Conservative:	22
Best Local Similarity:	30.81%	Mismatches:	80
Query Match:	21.53%	Indels:	44
DB:	2	Gaps:	6

US-09-847-102a-68 (1-235) x US-08-987-289-1 (1-2880)

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QY 33 CysGlnGluIleThValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 303 TGTGAACCAATTAATCTGTTCCAGATGTATGAAATGGCTTACACATGACGTTTTCCT 362

QY 53 AenglnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheThrPro 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 363 AATCTGATGGCTATTATATACCAAGACTATTTGCCGCGGTGAAATGAGCATTTTCTCT 422

QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThrPro 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 423 CTCGCAAACTCGAATGTTTACCAAAACATTGAACTTTCTCTCGCAAAACATTGTTGACA 482

QY 93 IleCysLeuProAspTyrHisIleAspLeuProProCysArgSerValCysGluArgAla 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 483 ACCTGATGAAACAAATTCAT---GTGGTTCACCTTGTCTGTTAACTTTGTGAGAAAGTA 539

QY 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaThrProGluArgMetSer 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 540 TATTTGATGCAAAAAATTAATATGACACTTTGGATGCCATGGCTGAGAGCTTGAA 599

QY 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 600 TGTGACAGATTACATACCTGTGATGAGACTGTTCCTGTA----- 638
  
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DB 467 CCTGGCTGAGATCCTCAATGCGATTAAGTTTCCT 502
RESULT 13
US-08-937-067-18
Sequence 18, Application US/08937067
Patent No. 643315
GENERAL INFORMATION:
APPLICANT: Melkonian, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-937-067-18
Alignment Scores:
Pred. No.: 9,91e-12 Length: 1308
Score: 240.50 Matches: 48
Percent Similarity: 49.32% Conservative: 25
Best Local Similarity: 32.43% Mismatches: 51
Query Match: 18.36% Indels: 24
Gaps: 4
DB: 4
US-09-847-102a-68 (1-235) x US-08-937-067-18 (1-1308)
QY 28 SerLyAlAProValCysGlnGluIle-----ThValProMetCysArgGlyIleGly 45
DB 458 ACCAAGCCACCTAGTGGCGGACATCCCGCGAGCTGGGGTGTGCCACACAGCGGGC 517
QY 46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeu 65
DB 518 TACAAGAGATGCTGCTGCCCACTGAGACAGACGACATGCGGAGGTGAAGACAG 577
QY 66 GluValHisGlnIleHetrProLeuValGluIleGlnCysSerProAspLeuAlaGlyPhe 85
DB 578 CAGGCGAGAGCTGGGGTCCCTGCTCAACAGAACTGCCACCGCGACCCAGGCTTC 637
QY 86 LeuCyMetMetYrThrProIleCysLeuProAspYrHisIleProLeuProProCys 105
DB 638 CTGTGCTGGCTTTCGCGCCCGCTGCTGCTG-----GACCGGCCCATCTACCGGTGT 688
QY 106 ArgSerValCysGlnIuArgAlaValAlaGlyCysSerProLeuMetArgIuGlyPhe 125

DB 689 CCGTGGCTCTGGAGCCCGTGGCGACATCGTCCGAGCCGCGTCAATGCAATTCCTGCGCTTC 748
QY 126 AlaTyrProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145
DB 749 TACTGCGCCGAGATGCTTAAGTGTACCAAGTTCCTC----- 784
QY 146 LeuCyMetAspTyrAsnArgSerGlu-AlaThrThrAlaProPro-----ArgProPh 163
DB 785 -----GAGGGGAGCTGTGCATGCGCATGACGCGGCCAAT 820
QY 163 eProAlaIleProThrLeuPro 170
DB 821 CCCAGGAGGCTCCAGCCCC 842
RESULT 14
US-09-276-531-16
Sequence 16, Application US/09276531
Patent No. 6183968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guebler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESSES:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITTT21
CLONE: 2526432
US-09-276-531-16
Alignment Scores:
Pred. No.: 4,46e-11 Length: 4245
Score: 240.50 Matches: 48
Percent Similarity: 49.32% Conservative: 25
Best Local Similarity: 32.43% Mismatches: 51

Query Match: 18.368 Indels: 24
 DB: 4 Gaps: 4
 US-09-847-102a-68 (1-235) x US-09-276-531-16 (1-4245)

QY 28 SerLeuValProValCysGlnGluLeu-----ThrValProMetCysArgGlyLeu 45
 DB 175 ACCAAGCCACTGACGCTGAGCATGCCCGGAGACTGCGGCTGTCACCAAGCTGGC 234
 QY 46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluVal 65
 DB 235 TACAGAGATGCTGCTGCCCAACTGCTGAGACAGACATGCGGAGGTGAAGCAG 294
 QY 66 GluValHisGlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhe 85
 DB 295 CAGGCGAGAGCTGGGTGCGCTGCTCAACAGAACTGCGAGCGGCGGACCCAGGCTTC 354
 QY 86 LeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLeuProLeuProCys 105
 DB 355 CTCTCTGCTCTGCTGCGCGCTGCTGCTG-----GACCGGCGCATCTACCGCTGT 405
 QY 106 ArgSerValCysGluArgAlaValAlaGlyCysSerProLeuMetArgGlnTyrGlyPhe 125
 DB 406 CCTGCGCTCTGCGAGCGCTGCGCACTGCTGCGAGCGGCTCATGCACTTCTGCTTC 465
 QY 126 AlaTrpProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145
 DB 466 TACTGCGCGAGATGCTTAACTGTGACAGAGTTCCTCC-----501
 QY 146 LeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro-----ArgProPh 163
 DB 502 -----GAGGGGAGGCTGCTGATGCGCATGACGCGGCGCAT 537
 QY 163 eProAlaValProThrLeuPro 170
 DB 538 GCCACCGAAGCTCCAGAGCC 559

RESULT 15
 US-08-893-654B-1
 ; Sequence 1, Application US/08893654B
 ; Patent No. 6165748
 ; GENERAL INFORMATION:
 ; APPLICANT: RACIE, LISA, ET ALIA
 ; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
 ; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CAMBRIDGE PARK DRIVE
 ; CITY: CAMBRIDGE
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140-2387
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/893,654B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEINERT, M.C.
 ; REGISTRATION NUMBER: 31,544
 ; REFERENCE/DOCKET NUMBER: GI 5279
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617.498.8574
 ; TELEFAX: 617.876.5851
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2190 base pairs
 ; TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 44..889
 US-08-893-654B-1

Alignment Scores:
 Pred. No.: 1,1e-10 Length: 2190
 Score: 231.50 Matches: 52
 Percent Similarity: 50.60% Conservative: 33
 Best Local Similarity: 30.95% Mismatch: 66
 Query Match: 17.67% Indels: 18
 DB: 4 Gaps: 5

US-09-847-102a-68 (1-235) x US-08-893-654B-1 (1-2190)

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 QY 27 ---AlaSerValProValCysGlnGluLeuThrValProMetCysArgGlyLeu 45
 DB 113 TCCACCAAGTGGCTTCCATTCCCAAGAGATGCC-----ATGTCAGATGACCTCGC 166
 QY 46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluVal 65
 DB 167 TACTGAGATGCGGCTTCCAACTGTTGGAGACACTTAACATGCGAAGTCTGCC 226
 QY 66 GluValHisGlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhe 85
 DB 227 AAGTACAGAGATGCGAGAACCTCTTACAGACCGGCTGCCACCTATGCCAGACTTC 286
 QY 86 LeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLeuProLeuProCys 105
 DB 287 CTATGCTCTCTTATTCGCCCGCAGTCTGCTGACACAGTTC-----ATCAGGCTGTC 337
 QY 106 ArgSerValCysGluArgAlaValAlaGlyCysSerProLeuMetArgGlnTyrGlyPhe 125
 DB 338 CGCAGCATGTGTTGCTGTAAGAAACAGTTGTGCTCCAGTTTGCGCATGTCATGGCAGC 397
 QY 126 AlaTrpProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145
 DB 398 TCTGCGCTGAGAGCTTGAAGTGAAGAGTTCAGCT-----GGGAGAGAC 445
 QY 146 LeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProProArgProPheProAla 165
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 QY 166 LysProThrLeuProGluProPro 173
 DB 499 AAGCCCAAGTGCAGGGGCTGCC 522

Search completed: May 22, 2003, 23:34:37
 Job time : 66 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 17:58:08 ; Search time 180 Seconds
(without alignments)
1723.937 Million cell updates/sec

Title: US-09-847-102A-68

Perfect score: 1310
Sequence: 1 MARPDPSAPSLLLLLLAQL.....PNCAPVCPYSPFSADERTFA 235

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09847102@cgn2.1.1.57@runat.19052003.160412.844
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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	2334	9	US-10-152-548-9
2	823.5	62.9	2421	9	US-10-152-548-15
3	754	57.6	424	10	US-09-867-701-6119
4	621	47.4	2344	9	US-10-152-548-1

Result No.	Score	Query Match	Length	ID	Description
5	440.5	33.6	2259	9	US-10-152-548-13
6	398	30.4	4540	10	US-09-917-800A-1684
7	378	28.9	1893	10	US-09-903-170C-10
8	378	28.9	1893	10	US-09-903-180B-10
9	378	28.9	1893	10	US-09-903-187A-10
10	378	28.9	1893	10	US-09-903-171A-10
11	378	28.9	1893	10	US-09-903-188A-10
12	378	28.9	1893	10	US-09-903-323A-10
13	378	28.9	1893	10	US-09-903-325A-10
14	372.5	28.4	1484	12	US-10-028-051-3
15	372.5	28.4	2039	9	US-09-974-228-16
16	372.5	28.4	2039	9	US-10-108-605-118
17	368.5	28.1	1291	9	US-10-090-049-23
18	367.5	28.1	1291	12	US-10-028-051-23
19	367.5	28.1	2176	9	US-09-903-170C-8
20	367	28.0	2176	10	US-09-903-180B-8
21	367	28.0	2176	10	US-09-903-187A-8
22	367	28.0	2176	10	US-09-903-171A-8
23	367	28.0	2176	10	US-09-903-188A-8
24	367	28.0	2176	10	US-09-903-323A-8
25	367	28.0	2176	10	US-09-903-325A-8
26	367	28.0	2176	10	US-10-090-049-1
27	366	27.9	2374	9	US-10-028-051-1
28	366	27.9	2374	12	US-09-903-170C-4
29	360	27.5	1875	9	US-09-903-180B-4
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31	360	27.5	1875	10	US-09-903-171A-4
32	360	27.5	1875	10	US-09-903-188A-4
33	360	27.5	1875	10	US-09-903-323A-4
34	360	27.5	1875	10	US-09-903-325A-4
35	360	27.5	1875	10	US-09-903-1775-1
36	358.5	25.8	2839	10	US-09-903-325A-4
37	308	23.5	2114	10	US-09-780-557-1
38	304.5	23.2	2624	9	US-10-152-548-3
39	300.5	22.9	484	9	US-09-918-985-23615
40	299.5	22.9	2828	9	US-10-152-548-7
41	284.5	21.7	885	9	US-09-934-483A-2
42	284.5	21.7	1799	9	US-09-934-483A-4
43	284.5	21.7	1859	9	US-09-934-483A-3
44	284.5	21.7	2030	9	US-10-146-474-1
45	284	21.7	2523	9	US-10-270-333-11

ALIGNMENTS

RESULT 1
US-10-152-548-9
Sequence 9, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Punima
Brink, Marcel
Wang, Yanshu
Heileh, Jen-Chih
Andrew, Deborah
Nathans, Jeremy
Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167,30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2334 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transmembrane receptor
(frizzled 5) mRNA, Coding region: 321..2078
US-10-152-548-9
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-152-548-9
Alignment Scores:
Pred. No.: 2,64e-120 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGlnLileThrValPromet 40
DB 381 GTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
QY 41 CysArgGlyTlIeGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
DB 441 TCCCGCGGCGATCGGCTACCAACCTGACGACGACATGCCAACCCAGTTCAACACGACGACG 500
QY 61 AspGluAlaGlyLeuGlnValHisGlnPheThrProLeuValGlnLileGlnCysSerPro 80
DB 501 GACGAGCGGCGGCTGAGGTCACCACTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCG 560
QY 81 AspLeuArgPhePheLeuLeuCysThrMetTyrThrProLileCysLeuProAspTyrHisLys 100
DB 561 GACCTCGGCTTCTCTCTATGCACTATGTCACCCCATCTGTCTGCCACCTACACCAAG 620
QY 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
DB 621 CCGCTCCGCGCGGCTCGGCTGAGGTCGAGCGGCGCAAGCGCGGCTGCTGCGGCTGAG 680
QY 121 ArgGlnTyrGlyPheAlaThrProGlnGlnMetSerCysAspArgLeuProValLeuGly 140
DB 681 CGCAGTACGCGCTTCCCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 740
QY 141 ArgAspAlaGlyValLeuLeuCysMetAspTyrAsnArgSerGlnLileThrAlaProPro 160
DB 741 CGGAGCGGCGGAGGTCCTTGTGATGATTACACCGACGAGCGGCGGCGGCGGCGGCGG 800
QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180

DB 801 AGGCTTTCCAGCCAGCCACCTTCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 860
QY 181 GlnCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProLileLeu 200
DB 861 GATGCGCGGCTGGGCGGCGGCTGCTGAGTGTGCGGAGCTTGTGCTGCTGCTGCTGCTG 920
QY 201 LysGlnSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
DB 921 AAGGAGTACACCCGCTTACACAAAGGTGGGACGGGCGGAGTGTGCTGCTGCTGCTGCTG 980
QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB 981 CCTGCTACACAGCGCTTCTTCACTGTCGACGACGACGACGACGCTTCTGCC 1025
RESULT 2
US-10-152-548-15
Sequence 15, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
Brink, Marcel
Harryman, Cindy S.
Wang, Yanshu
Hsieh, Jen-chih
Andrew, Deborah
Nathans, Jeremy
Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167,30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2421 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Mus musculus transmembrane receptor
(frizzled 8) gene, Coding region: 188..2245
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-152-548-15


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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2344 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Dfz2 Polynucleotide, coding region
begin at nucleotide #225
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-152-548-1

Alignment Scores:
Score: 3,34e-52 Length: 2344
Percent Similarity: 621.00 Matches: 124
Best Local Similarity: 52.80% Conservative: 27
Query Match: 47.40% Mismatches: 55
DB: 9 Indels: 80
Gaps: 7

US-09-847-102a-68 (1-235) x US-10-152-548-1 (1-2344)
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QY 32 -----ValCysGlnGluIleThrValProMetCysArgGlyIleGlyIleThrValLeu 48
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QY 109 C|y|G|I|U|A|I|A|L|y|A|a|G|I|U|C|y|S|e|P|r|o|L|e|u|M|e|T|A|R|G|I|N|T|Y|G|I|U|P|H|e|A|T|P|P|o| 128

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DB 623 G|A|G|A|A|T|G|G|C|T|G|G|A|G|A|C|T|T|G|C|C|T|C|A|T|G|T|-----G|A|C|C|C|G|A|C|A|T|T|G|T|G|C|A|T|G| 679
QY 149 A|s|P|T|Y|----- 150
DB 680 G|A|A|C|A|G|C|C|C|T|G|T|A|C|A|C|G|A|G|G|T|G|G|C|G|G|T|G|G|C|A|G|C|T|G|G|G|G|A|T|G|G|G|T|G|T|C|T| 739
QY 150 ----- 150
DB 740 G|G|C|A|G|G|T|T|C|G|G|T|C|C|G|G|G|G|C|A|A|C|G|A|A|G|C|A|G|A|G|C|A|G|C|A|G|T|G|C|T|G|G|G|C|G|C|A|G|T| 799
QY 151 -----A|s|n|A|S|e|r|G|I|U|A|I|H|T|H|A|P|r|o|P|r|o|A|R|P|r|o|P|H|e|P|r|o|A|I|A|Y|S| 166
DB 800 G|G|G|G|C|C|G|G|G|C|G|C|A|G|A|G|G|G|T|T|C|C|A|C|C|T|C|A|C|A|G|C|C|G|T|G|C|G|G|G|A|C|G|C|A|T|T|C|A|A|A| 859
QY 167 P|r|o|T|H|L|e|u|P|r|o|G|I|Y|P|r|o|G|I|Y|A|L|P|r|o|A|I|S|e|r|G|I|Y|G|I|U|C|y|S|e|P|r|o|A|I|G|I|Y|G|I| 186
DB 860 ---A|A|C|T|G|C|A|A|A|T|C|C|C|C|A|G|A|A|A|G|C|A|A|G|C|G|A|A|A|G|A|G|T|G|C|A|G|C|----- 907
QY 187 P|r|o|P|H|e|V|a|I|C|y|S|e|C|y|A|R|G|I|U|P|r|o|P|H|e|V|a|I|----- 197
DB 908 -----T|G|C|T|G|T|G|C|C|T|C|C|C|A|C|T|C|A|T|C|T|T|C|T|G|G|G|G|A|A|G|A|C|A|C|A|C|A|G|C|T|G|C|A|G| 958
QY 198 -----P|r|o|I|L|e|u|I|S|G|L|u|S|e|r|H|I|S|P|r|o|L|e|u|Y|A|s|n|I|Y|A|I|----- 210
DB 959 C|A|G|C|A|G|T|G|C|A|G|A|T|C|C|A|T|A|T|G|C|A|C|A|T|C|A|C|A|C|C|A|C|A|C|T|G|T|A|T|A|A|C|T|A|C|T|G|T|C| 1018
QY 211 ---A|r|G|T|H|G|I|U|A|I|P|r|o|A|s|n|C|y|S|A|I|A|V|A|I|P|r|o|C|y|S|T|Y|G|I|N|P|r|o|S|e|P|H|e|S|e|A| 229
DB 1019 C|A|A|A|G|A|T|G|C|G|G|G|G|T|T|C|A|A|A|C|T|G|C|G|C|A|T|A|C|C|G|C|A|A|G|G|G|C|C|T|T|C|A|G|A|C| 1078
QY 230 A|s|P|G|I|U|A|R|G|I|U|P|H|e|A|I| 235
DB 1079 G|A|C|G|A|A|A|G|A|T|T|G|C|C| 1096

RESULT 5
US-10-152-548-13
Sequence 13, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
Brink, Marcel
Harryman, Cindy S.
Wang, Yanshu
Heiren, Jen-chih
Andrew, Deborah
Nathans, Jeremy
Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307

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QY 73 LeuValGluIleGlnCysSerProAspLeuArgPheLeuCysThrMetYrThrPro 92
DB 1216 TTGGTGAAGAGTCTCAGAGCTCAGAGCTCAAGTTCTTCTGCTGCTCAATGATACGGCCCT 1275
QY 93 IleCysLeuProAspYrThrIleSyrProLeuProProCysArgSerAlaCysGluAla 112
DB 1276 GGTGTGACCGTA--CTGAGACAGGCGCTGCTCTCCCTGCGCTGCTGCGAGCGCGCC 1332
QY 113 LysAlaGlyCysSerProLeuMetArgGlnYrGlyPheAlaTrpProGluArgMetSer 132
DB 1333 CAG---GGTGTGAGAGCACTCATGAACAAGTTCCAGTCCAGTGGCCAGACAGCTCAAG 1389
QY 133 CysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMetAspYrTranArg 152
DB 1390 TCGAGAAAGTCCCTTGTGACAGCGC-----GCAGAGAGCTGTGCTGGGCGCAAGAACT 1443
QY 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
DB 1444 TCCGACAAAGGACCCCGACTCCCTCTGCTGCTGCGAGTTCTGACCAAGATCCGCGAG 1503
QY 173 ProGlyAlaProAlaSerGlyGlyGlyCysProAlaGly-----Gly 186
DB 1504 CACGGGGGGGTGTTACCGCGCGGCTACCGGAGAGTGCAGCCCGCGGAGCGGGA 1563
QY 187 PropheValCysLysCysArgGluProPheValProIleLeuLysGluSerHisProLeu 206
DB 1564 AAGTTCTCTGCGCG--CGCGCCCTCAGAGTGCCTTCTTCACTCAATATCATCTTTCTG 1620
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysYrGlnProSer 226
DB 1621 GGGGAGAG-----PheSerAlaAspGluArgThrPheAla 235
QY 227 ----- 1657 AAAGTTACGGGCTCATGTACTTCCGGCCTGAGAGTAATTCGCTTTTCG 1704

RESULT 7
US-09-903-170C-10
; Sequence 10, Application US/09903170C
; Patent No. US20020156249A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-259
; CURRENT APPLICATION NUMBER: US/09/903,170C
; PRIORITY FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
US-09-903-170C-10

Alignment Scores:
Pred. No.: 2,71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-170C-10 (1-1893)
QY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeu 17
DB 40 CCGTCCCATCTTCGCGGATCATGTCTGCGGAGCGCGGAGAGGATGCTGCTGCTGCGG 99
QY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31

```

```

DB 100 GCCGGGCGCTTGCCTGCTGCTCTCTGCTCTCCAGGTGCCGGGGCTTGGGCTGCA 159
QY 32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
DB 160 GCTGTGAGCCCGTCCGATCTCCCTGTGCAAGTCCCTCCCTGGAACATGATCAAGT 219
QY 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
DB 220 CCCAACCACTGACACCAACAGACCTGAGCCCAAGCCATCTGCGCATGAGACGATTCGAA 279
QY 72 ProLeuValGluIleGlnCysSerProAspLeuArgPheLeuCysThrMetYrThr 91
DB 280 GGTCTGCTGGGACACCACCTGAGCGCCCATCTGCTTCTTCTTGTGCGCATGACGCG 339
QY 92 ProIleCysLeuProAspYrThr--HisLysProLeuProProCysArgSerValCysGlu 110
DB 340 CCCATCTGACCATTTGACTTCCAGACAGACCCATCAAGCCCTGTAAAGTCTGTGCGAG 399
QY 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnYrGlyPheAlaTrpProGluArg 130
DB 400 CGGGCCGAGAGGCTGTGAGCCCATCTCATCAAGTACCGCCACTCGTGGCGGAGAAC 459
QY 131 MetSerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMetAspYr 150
DB 460 CTGGCTCGAGAGAGCTCCAGTGTACAGACAGGGGC-----GTGTGATC----- 504
QY 151 AsnArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 170
DB 505 TCTCCGAGGCCATGTTACTGCGAGCGAGCTGATTTTCT----- 546
QY 171 GlyProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyProPheValCys 190
DB 547 -----ATGATTTCTAGTACGAAACTGTAGAGGGGCAAGACGTAAACGCTGT 594
QY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeu----- 206
DB 595 AAATGTAG-----CCTATTAGAGCTACACAGAAAGACTATTTCGGAACAAT 642
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysYr 223
DB 643 TACAATCTATGTCATTCGGGCTTAAAGTAAAGATTAAGACTTAAGTGCAT 693

RESULT 8
US-09-903-180B-10
; Sequence 10, Application US/09903180B
; Patent No. US20020099171A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-256
; CURRENT APPLICATION NUMBER: US/09/903,180B
; PRIORITY FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
US-09-903-180B-10

Alignment Scores:
Pred. No.: 2,71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
Gaps: 8

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US-09-847-102A-68 (1-235) X US-09-903-180B-10 (1-1893)

QY	ProAspProSerLysIle-----ProProSerLeuLeuLeuLeuLeu	17
Db	40 CTTGCCCACTCTGCGGGATCATGCTCTCGGACGCCGAGGAGTCTGCTGCGG	99
QY	18 AlaGlnLeuValGluValGlnAlaAla-----AlaAlaSerLysAlaPro	31
Db	100 GCGGGGCTGCTCCCTCGGCTGCTCTCTGCTCGCTCGGCTCCCGGGGCTCGGGCTTGTCA	150
QY	32 ValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet	51
Db	160 GCGCTGTAGCCCTCCGCGCATCCCTCGTGCAGATGCCCTGCGAAGATACATAAGATG	219
QY	52 ProAsnGlnHisAsnHisAspThrGlnIleAspGluValGlnLeuValHisGlnPheTrp	71
Db	220 CCCAACACACTGACACACAGACTCGGGCAACGCCATCTCTGGCCATGAGCAGCTTGGAA	279
QY	72 ProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThr	91
Db	280 GGTCTGTGTGGGACCCACCTGACGCCCTCTCTCTCTGTCGTCATGACGCG	335
QY	92 ProIleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGln	110
Db	340 CCATCTGCACCACTATGACTTCCAGACGAGGCCATCAAGCCCTGTAAAGTCTGTGGGAG	399
QY	111 ArgAlaLysValaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGlnArg	130
Db	400 CGGGCCCGGAGGGGCTGTGAGCCCAATACATCACTAGTACCGGCACCTCGTGGCCGGAGAC	458
QY	131 MetSerCysAspArgLeuProValLeuGluArgAspAlaGluValLeuCysMetCysAspTyr	150
Db	460 CTGGCTGCGCAGAGCTGCGCAGTACGACAGGGGC-----GTGTGATC-----	504
QY	151 AsnArgSerGlnIleThrThrAlaProProArgProPheProAlaLysProThrLeuPro	170
Db	505 TCTCCGAGGCCATCTGTACTGTCGGACGAGACTGATTTTCC-----	546
QY	171 GlyProProGluValaProAlaSerGlyGlyGlnCysProAlaGlyLysProPheValCys	190
Db	547 -----ATGATTTCTAGTACGAAACTGAGGGGCGAAGCAGTGAACGGCTGT	594
QY	191 LysCysArgGlnLysProPheValProIleLeuLysGlnSerHisAspLeu-----	206
Db	595 AAATGTAAAG-----CCTATTAGCTACACAGAAAGACTTATTCGGAAACAT	642
QY	207 TyrAsnLysValaArgThrGlyGlnValProAsnGlyAlaValProCysTyr	223
Db	643 TACACATATATCTATTGGGCTTAAAGTTAAAGATTAAGATTAAGACTTAAGTGCAT	693

ORGANISM: Human
US-09-903-187A-10

Alignment Scores:	
Pred. No.:	2, 71e-28
Score:	378.00
Percent Similarity:	49.79%
Best local Similarity:	35.44%
Query Match:	28/85
DB:	10
Length:	1899
Matches:	84
Conservative:	34
Mismatches:	83
Indels:	36
Gaps:	8

US-09-847-102A-68 (1-235) x US-09-903-187A-10 (1-1893)

```

Oy      4 ProAspProSerAla-----ProPseSerLeuLeuLeuLeuLeu 17
Db      40 CCGGCCCATCTGCGGGATATGTTCTGCGGACGCCGGAGGAGTGTGTCGTCGCG 99

Oy      18 AlaGlnLeuValGlyArgAlaA-----AlaAlaSerLybAlPro 31
Db      100 GCGGGGCTCTGCCTCCCTGCTCTCTCTGCTCTGCGGTGCCGGGGCTCGGGCTGCA 159

Oy      32 ValCyegInGluIleThrValProMetCysArgGlyIleGlyTrpAnLeuThnIleMet 51
Db      160 GCCTGTGAACCCGTCCGCATCCCCCTTGCCAAGTCCCTGCTGAAACAATAAATG 219

Oy      52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHISglnPheTrp 71
Db      220 CCCAACCACTGACACACAGACACTGACGGCCAAACGGCATCTGGCCATCGACAGATTGAA 279

Oy      72 ProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCyethrMetTyThr 91
Db      280 GGCTCTCTGGGACCACCGACGACGCCCATGTGCTCTTCCCTGTGCGCATGTACGCG 339

Oy      92 ProIleCysLeuProAspTyr---HisLysPProleuProProCysAsGSerValCysGlu 110
Db      340 CCATCTGCACCATTAATGACTTCCAGACACAGCCCATCAAGCCCTTAAGTCTGTGTGCGAG 399

Oy      111 ArgAlaLybAlaGlyCysSerProLeuMetArgGlnTyrglyPheaIatProGluArg 130
Db      400 CGGGCCGGGACGGGCTGTGAGCCCATCTCATCAAGTACCGGCACACTGTCGGCCGAGAAC 459

Oy      131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
Db      460 CTGGCTCTGGAGAAGCTGCCAGETGACACAGCGGGC-----GTTGTGATC----- 504

Oy      151 AsnArgSerGluAlaThrThralapProProArgProPheProAlaLysProThrlauPro 170
Db      505 TCTCCCGAGCCATGCTTACTGCGGACGGAGCTGATTTTCT----- 546

Oy      171 GlyProGluYalaProAlaSerGlyGlyLucCysProAlaGlyglyProPheValCys 180
Db      547 -----ATGATATTCTAGTAAACGAAACTGTADAGGGGACAGACAGTGAACGCTGT 594

Oy      191 LysCyArgGluProPheValProIleLeuLybGluSerHisPProleu----- 206
Db      595 AAATGTAAAG-----CCTATTGAGACTACACAGAACCTATTTCGGAACAAAT 642

Oy      207 TyrAsnLybValArgThrGlyGluValProAsnCysAlaValProCysTyR 223
Db      643 TACAACTAATGTCAATTCGGGCTAAAGTTTAAAGAGATAAAGACTAAGTGCAT 693

RESULT 10
US-09-903-171A-10
; Sequence 10, Application US/09903171A
; Patent No. US20020123613A1
GENERAL INFORMATION:
; APPLICANT: De Roderis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-260
; CURRENT APPLICATION NUMBER: US/09/903,171A
; CURRENT FILING DATE: 2001-07-11
```

; PRIOR APPLICATION NUMBER: US 60/020,150
 ; PRIOR FILING DATE: 1996-06-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Human FR2B-1
 US-09-903-171A-10

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2.71e-28	1893	84	34	83	36	8
Percent Similarity: 49.79%						
Best Local Similarity: 35.44%						
Query Match: 28.85%						

US-09-847-102A-68 (1-235) x US-09-903-171A-10 (1-1893)

```

OY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeu 17
    |||||
DB 40 CCGGCCCATCTGCGCGGATCATGCTCTGCGGAGCGCGGAGGATGCTGCTGCGG 99
    |||||
OY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
    |||||
DB 100 GCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159
    |||||
OY 32 ValCysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
    |||||
DB 160 GCGTGGAGCCCGCTGCGCATCCCTGTCGCAAGTCCCTGCGCAACATGACTAAGATG 219
    |||||
OY 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
    |||||
DB 220 CCCAACCACTGACACCAACAGCACTACAGCCCAAGCCATCTGCGCATGACAGATTGCA 279
    |||||
OY 72 ProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91
    |||||
DB 280 GGTCTGCTGGGACCCACCTGACGACCCCGATCTCTCTTCTCTGTCGTCATGATGCG 339
    |||||
OY 92 ProIleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGlu 110
    |||||
DB 340 CCCATCTGACACCATTACTTCACAGACGAGCCCATCAAGCCCTGTAACTGTGTGCGAG 399
    |||||
OY 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArg 130
    |||||
DB 400 CGGCGCCCGGAGGCGCTGTAGCCCATATCATCAAGTACCGCCACTGTCGCGGAGAAC 459
    |||||
OY 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
    |||||
DB 460 CTGGCTGCGAGAGAGCTGCGACAGTGTACGACAGGGGC-----GTGTGTCATC----- 504
    |||||
OY 151 AsnArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 170
    |||||
DB 505 TCTCCCGAGGCGCATCTTACTGCGAGCGAGCTGATTTCCT----- 546
    |||||
OY 171 GlyProProGlyValAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCys 190
    |||||
DB 547 -----ATGATTTCTAGTAACGAACTGTAGAGGGGCAAGCAGTGAACGCTGT 594
    |||||
OY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeu----- 206
    |||||
DB 595 AAATGTAAAG-----CCTATTAGAGTAAACAGAAAGACTATTTCGGAACAAT 642
    |||||
OY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
    |||||
DB 643 TACAACTAGTCAATTCGGGCTAAAGTTAAAGATAAAGACTAAGTCAAT 693
    |||||

```

RESULT 11

; Sequence 10, Application US/09903188A
 ; Patent No: US20020128439A1
 ; GENERAL INFORMATION:

; APPLICANT: De Robertis, Edward M.
 ; APPLICANT: Bouwmeester, Tewis
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; TITLE OF INVENTION: Factors
 ; FILE REFERENCE: 510015-258
 ; CURRENT APPLICATION NUMBER: US/09/903,188A
 ; CURRENT FILING DATE: 2001-07-11
 ; PRIOR APPLICATION NUMBER: US 60/020,150
 ; PRIOR FILING DATE: 1996-06-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Human FR2B-1
 US-09-903-188A-10

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2.71e-28	1893	84	34	83	36	8
Percent Similarity: 49.79%						
Best Local Similarity: 35.44%						
Query Match: 28.85%						

US-09-847-102A-68 (1-235) x US-09-903-188A-10 (1-1893)

```

OY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeu 17
    |||||
DB 40 CCGGCCCATCTGCGCGGATCATGCTCTGCGGAGCGCGGAGGATGCTGCTGCGG 99
    |||||
OY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
    |||||
DB 100 GCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159
    |||||
OY 32 ValCysGlnGluLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
    |||||
DB 160 GCGTGGAGCCCGCTGCGCATCCCTGTCGCAAGTCCCTGCGCAACATGACTAAGATG 219
    |||||
OY 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
    |||||
DB 220 CCCAACCACTGACACCAACAGCACTACAGCCCAAGCCATCTGCGCATGACAGATTGCA 279
    |||||
OY 72 ProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91
    |||||
DB 280 GGTCTGCTGGGACCCACCTGACGACCCCGATCTCTCTTCTCTGTCGTCATGATGCG 339
    |||||
OY 92 ProIleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGlu 110
    |||||
DB 340 CCCATCTGACACCATTACTTCACAGACGAGCCCATCAAGCCCTGTAACTGTGTGCGAG 399
    |||||
OY 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArg 130
    |||||
DB 400 CGGCGCCCGGAGGCGCTGTAGCCCATATCATCAAGTACCGCCACTGTCGCGGAGAAC 459
    |||||
OY 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyr 150
    |||||
DB 460 CTGGCTGCGAGAGAGCTGCGACAGTGTACGACAGGGGC-----GTGTGTCATC----- 504
    |||||
OY 151 AsnArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 170
    |||||
DB 505 TCTCCCGAGGCGCATCTTACTGCGAGCGAGCTGATTTCCT----- 546
    |||||
OY 171 GlyProProGlyValAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCys 190
    |||||
DB 547 -----ATGATTTCTAGTAACGAACTGTAGAGGGGCAAGCAGTGAACGCTGT 594
    |||||
OY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeu----- 206
    |||||
DB 595 AAATGTAAAG-----CCTATTAGAGTAAACAGAAAGACTATTTCGGAACAAT 642
    |||||
OY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
    |||||

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Db 643 TACAACCTATGTCATTCCGGCTAAAGTAAAGATTAAGACTTAAGTCCCAT 693

RESULT 12

US-09-903-323A-10

Sequence 10, Application US/09903323A

Patent No. US20020128440A1

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

APPLICANT: Boumeester, Lewis

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

TITLE OF INVENTION: Factors

FILE REFERENCE: 510015-261

CURRENT APPLICATION NUMBER: US/09/903,323A

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10

LENGTH: 1893

TYPE: DNA

ORGANISM: Human FRZB-1

US-09-903-323A-10

Alignment Scores:

Pred. No.: 2,71e-28 Length: 1893

Score: 378.00 Matches: 84

Percent Similarity: 49.79% Conservative: 34

Best Local Similarity: 35.44% Mismatches: 83

Query Match: 28.85% Indels: 36

DB: 10 Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-323A-10 (1-1893)

QY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeu 17

Db 40 CTGCCCCATCTGCGGGATCATGTCGCGGACCCGGAGGAGATGCTGCTGCGG 99

QY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerIyAlaPro 31

Db 100 GCCGGGCTGCTGCGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159

QY 32 ValCyGlnGlnIleThrValProMetCysArgGlyIleGlyIYrAsnLeuThrHisMet 51

Db 160 GCGCTGTAGCCCTGCGATCCCTGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTG 219

QY 52 ProAsnGlnPheAsnHisAspThrGlnAspGlnIleGlyLeuGlnValHisGlnPheTrp 71

Db 220 CCCAACCACTGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 279

QY 72 ProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91

Db 280 GGTCTGCTGGGACCCACTGACGACGACGACGACGACGACGACGACGACGACGACGACG 339

QY 92 ProIleCysLeuProAspYr---HisIySProLeuProProCysArgSerValCysGln 110

Db 340 CCCATCTGACACCATTTGATCTTCCAGACGACGACGACGACGACGACGACGACGACG 399

QY 111 ArgAlaIyAlaGlyCysSerProLeuMetArgGlnIYrGlyPheAlaTrpProGluArg 130

Db 400 CGGGCCCGGACGAGGCTGTGAGCCCATCTGATCATCATCATCATCATCATCATCATCAT 459

QY 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMetAspYr 150

Db 460 CTGGCTGCGAGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504

QY 151 AsnArgSerGlnIleThrThrAlaProArgProPheProAlaIleYsProThrLeuPro 170

Db 505 TCTCCCGAGGCGCATGTTACTGCGAGCGAGCTGATTTTCTT-----GTGTGATC----- 546

QY 171 GlyProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyIYrProPheValCys 190

Db 547 -----ATGATTTCTAGTAACGAACTGTAGAGGGGCAAGCAGTGAACGCTGT 594

QY 191 LysCysArgGlnProPheValProIleLeuIySglnSerHisProLeu----- 206

Db 595 AAATCTAG-----CCTATTAGACTACACAGAGACTATTTCGGAACAT 642

QY 207 TyrAsnIySValArgThrGlyGlnValProAsnCySAlaValProCysYr 223

Db 643 TACAACCTATGTCATTCCGGCTAAAGTAAAGATTAAGACTTAAGTCCCAT 693

RESULT 13

US-09-903-325A-10

Sequence 10, Application US/09903325A

Patent No. US20020128441A1

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

APPLICANT: Boumeester, Lewis

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

TITLE OF INVENTION: Factors

FILE REFERENCE: 510015-257

CURRENT APPLICATION NUMBER: US/09/903,325A

CURRENT FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10

LENGTH: 1893

TYPE: DNA

ORGANISM: Human FRZB-1

US-09-903-325A-10

Alignment Scores:

Pred. No.: 2,71e-28 Length: 1893

Score: 378.00 Matches: 84

Percent Similarity: 49.79% Conservative: 34

Best Local Similarity: 35.44% Mismatches: 83

Query Match: 28.85% Indels: 36

DB: 10 Gaps: 8

US-09-847-102A-68 (1-235) x US-09-903-325A-10 (1-1893)

QY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeu 17

Db 40 CTGCCCCATCTGCGGGATCATGTCGCGGACCCGGAGGAGATGCTGCTGCGG 99

QY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerIyAlaPro 31

Db 100 GCCGGGCTGCTGCGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159

QY 32 ValCyGlnGlnIleThrValProMetCysArgGlyIleGlyIYrAsnLeuThrHisMet 51

Db 160 GCGCTGTAGCCCTGCGATCCCTGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTG 219

QY 52 ProAsnGlnPheAsnHisAspThrGlnAspGlnIleGlyLeuGlnValHisGlnPheTrp 71

Db 220 CCCAACCACTGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 279

QY 72 ProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91

Db 280 GGTCTGCTGGGACCCACTGACGACGACGACGACGACGACGACGACGACGACGACGACG 339

QY 92 ProIleCysLeuProAspYr---HisIySProLeuProProCysArgSerValCysGln 110

Db 340 CCCATCTGACACCATTTGATCTTCCAGACGACGACGACGACGACGACGACGACGACG 399

QY 111 ArgAlaIyAlaGlyCysSerProLeuMetArgGlnIYrGlyPheAlaTrpProGluArg 130

Db 400 CGGGCCCGGACGAGGCTGTGAGCCCATCTGATCATCATCATCATCATCATCATCATCAT 459

QY 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMetAspYr 150

Db 460 CTGGCTGCGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504

QY 151 AsnArgSerGluAlaThrThrAlaProPheProAlaLysProThrLeuPro 170
Db 505 TCTCCGAGCCATCGTTCGCGAGCGAGCGATTTCTCT----- 546
QY 171 GlyProGlyAlaProAlaSerGlyGlyCysProAlaGlyLysProPheValCys 190
Db 547 -----ATGATTCCTAGTAAAGAACTGTAGAGGGGCAAGCAAGCGCTGT 594
QY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTAAG-----CCTATTAGAGCTACAGAAAGCCTATTTCGGAACAT 642
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
Db 643 TACAACTACTGTCATTCGGGCTAAAGTTAAAGATTAAGACTAAGTGGCCAT 693
RESULT 14
US-10-090-049-3
Sequence 3, Application US/10090049
Publication No. US20030009023A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Malcolm
APPLICANT: Hoang, Bang
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: ISOLATION AND METHOD OF USING TISSUE
FILE OF INVENTION: GROWTH-INDUCING FRZB PROTEIN
CURRENT APPLICATION NUMBER: US/10/090,049
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 09/289,268
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: PCT/US97/18362
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: US 08/822,333
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1484
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-090-049-3
Alignment Scores:
Pred. No.: 7.14e-28 Length: 1484
Score: 372.50 Matches: 82
Percent Similarity: 49.58% Conservative: 35
Best Local Similarity: 34.75% Mismatches: 84
Query Match: 28.44% Indels: 35
Gaps: 8
US-09-847-102a-68 (1-235) x US-10-090-049-3 (1-1484)
QY 4 ProAspProSer-----AlaProProSerLeuLeuLeuLeuLeuAla 18
Db 190 CCCATCTCTGCGCGGATCATGCTCTCGCGAGCGCGAGGATGCTGCTGCGCGGCC 249
QY 19 GlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaProVal 32
Db 250 GGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
QY 33 CysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
Db 310 TGGAGCCCGCTCGCATCCCGCTGCTCAAGTCCCTCGGAACATGACTAGATGCCCC 369
QY 53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGlnValHisGlnPheTyrPro 72
Db 370 AACCACTGACACACAGCATCTAGGCCAACGCCATCTGCCATCGACAGTTGCAAGT 429
QY 73 LeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro 92

Db 430 CTGCTGGGACACCCACTGACGAGCCCATCTGCTCTTCTCTGCGCATGACCGGCC 489
QY 93 IleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGlnArg 111
Db 490 ATCTGCACCATTTAGCTTCAGACGAGCCCATCAAGCCCTGTAACTGTGTGTGCGAGCG 549
QY 112 AlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGluArgMet 131
Db 550 GCCCGGACGGGCTGTGAGCCCATCTACTCATCAAGTACCCGCACTGTCGCGGAGAACTG 609
QY 132 SerCysAspArgLeuProValLeuGlnValArgAspAlaGluValLeuCysMetAspTyrAsn 151
Db 610 GCCTCGGAGGAGCTCCAGATGACGACAGGGGC-----GTGTGCATC-----TCT 654
QY 152 ArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGly 171
Db 655 CCGAGGCCCATCTGTCAGCGGAGCGAGCTGATTTCT----- 693
QY 172 ProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyLysProPheValCysLys 191
Db 694 -----ATGATTCCTAGTAAAGAACTGTAGAGGGGCAAGCAAGTAAAGCTGTA 744
QY 192 CysArgGluProPheValProIleLeuLysGluSerHisProLeu-----Tyr 207
Db 745 TGTAA-----CCTATTAGAGCTACACAGAAAGCCTATTTCGGAACATTAAC 792
QY 208 AsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
Db 793 AACATGTCATTCGGGCTAAAGTTAAAGATTAAGACTAAGTGGCCAT 840
RESULT 15
US-10-028-051-3
Sequence 3, Application US/10028051
Patent No. US20020147329A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Hoang, Bang
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
FILE OF INVENTION: GROWTH INDUCING FRZB PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/028,051
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,452
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 39,901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 base pairs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_p1us_p2n model

Run on: May 22, 2003, 19:43:08 ; Search time 1516 Seconds
(without alignments)
2510.514 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPDPSAPSLILLLLAQL.....PNCAPVCYQPSFSADERTFA 235

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US09847102/runat_19052003_160406_736/app_query.faacta_1.391
-DB=EST -QFMT=fastap -SUPFIX=est -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=DCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09847102.GCGN 1.1.1906 @runat_19052003_160406_736 -NCPU=6 -ICPU=3
-NO MMAP -LARGEBUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hcc:*
9: gb_estc1:*
10: gb_estc2:*
11: gb_hcc:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_esthum:*
16: em_esthum:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	880	67.2	492	12 BE953717	BE953717 UI-M-CC1-AA481448 zva5b07.8
2	754	57.6	424	9 AA481448	AA481448 Telereodon
3	653.5	49.9	1028	17 CNS02Z0H	AL221426 Telereodon
4	652	49.8	653	10 BB625724	BB625724 BB622817
5	618.5	47.2	635	10 BB622817	BB622817 BB622817
6	584	44.6	457	10 AA462410	AA462410 BP230009A
7	567	43.3	564	17 AZ475021	AZ475021 IM0292116
8	534.5	40.8	564	12 BG438433	BG438433 p25d03.y
9	524.5	40.0	559	12 BG353236	BG353236 p25d03.y
10	513	39.2	603	9 A1892150	A1892150 mh41e05.y
11	502.5	38.4	571	12 BE718107	BE718107 RCI-HT079
12	477	36.4	679	9 A1958244	A1958244 fd02c05.y
13	461	35.2	607	10 BB619404	BB619404 BB619404
14	440	33.6	580	9 A1860140	A1860140 wh39f09.x
15	427.5	32.6	536	12 BF434722	BF434722 7p03e09.x
16	419	32.0	937	14 BQ725011	BQ725011 AGENCOURT
17	418	31.9	894	14 BQ736171	BQ736171 AGENCOURT
18	417.5	31.9	658	9 AL651565	AL651565 AL651565
19	414.5	31.6	580	13 B1444839	B1444839 dae79a04.y
20	411.5	31.4	1138	14 BM905248	BM905248 AGENCOURT
21	408.5	31.2	957	14 BQ231687	BQ231687 AGENCOURT
22	408	31.1	535	13 B107483	B107483 B107483
23	401.5	30.6	934	14 BQ651465	BQ651465 AGENCOURT
24	399	30.5	595	9 A1794418	A1794418 fc44b09.y
25	398	30.4	494	9 AA017737	AA017737 mh41e05.x
26	397.5	30.3	375	9 AV193231	AV193231 AV193231
27	396.5	30.3	918	14 BQ650644	BQ650644 AGENCOURT
28	394.5	30.1	857	14 BQ650917	BQ650917 AGENCOURT
29	394.5	30.1	1086	14 BM927842	BM927842 AGENCOURT
30	393.5	30.0	360	14 C46856	C46856 C46856 yu11
31	393.5	30.0	572	9 A1437185	A1437185 fb38g02.y
32	391.5	30.0	2294	11 AK021164	AK021164 Mus muscu
33	391.5	29.9	983	14 BQ645792	BQ645792 AGENCOURT
34	389.5	29.7	1232	14 BQ644208	BQ644208 AGENCOURT
35	386.5	29.5	360	14 C49875	C49875 C49875 yu11
36	383.5	29.3	1317	14 BQ645492	BQ645492 AGENCOURT
37	382.5	29.2	1030	14 BQ647904	BQ647904 AGENCOURT
38	382	29.2	213	9 AA023595	AA023595 mh80d03.x
39	381.5	29.1	360	9 AV190346	AV190346 AV190346
40	381.5	29.1	360	14 C39586	C39586 C39586 yu11
41	381	29.1	891	17 CNS04S34	AL304681 Telereodon
42	379.5	29.0	417	9 A1545106	A1545106 fb70g09.y
43	379	28.9	1083	14 BQ653826	BQ653826 AGENCOURT
44	377	28.8	610	13 B1556566	B1556566 603239542
45	376.5	28.7	376	14 C39238	C39238 C39238 yu11

ALIGNMENTS

RESULT 1
LOCUS BE953717 492 bp mRNA linear EST 29-APR-2002
DEFINITION UI-M-CC1-gzx-c-04-0-UI.s1 NIH BMP Recl N Mus musculus cDNA clone
ACCESSION BE953717
VERSION BE953717.1 GI:10595515
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 492)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

discovery.
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov

Oligo-dt track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine
Seq primer: M13 Forward
POLYA=No.

FEATURES

Location/Qualifiers
1..492
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U1-M-CCI-azx-C-04-0-UI"
/clone_1lb="NIH_BMAP_Recl_N"
/dev_stage="13.5 days pc"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_Recl_N library is a normalized library derived
from NIH_BMAP_Recl_N. NIH_BMAP_Recl was made from mouse embryonic
retina tissue. For a detailed description of the library
from which this clone was derived, please visit our web
site at brainest.eng.umd.edu. The tissue for this
library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TMG_SRO=None found"

BASE COUNT 87 a 182 c 138 g 85 t
ORIGIN

Alignment Scores:

Pred. No.: 1,95e-63 Length: 492
Score: 880.00 Matches: 154
Percent Similarity: 97.538 Conservative: 4
Best Local Similarity: 95.064 Mismatches: 0
Query Match: 67.184 Indels: 0
DB: 12 Gaps: 0

US-09-847-102a-68 (1-235) x BE953717 (1-492)

QY 26 AAlaASeLyAlaProValCySGInGluIleThValProMetCysArgGlyIleGly 45
DB 3 GCCGCTCCAAAGGCCCGGCTGTGCCAGGAATACCGGTGCCATGTGCCAGGCGATCGCG 62
QY 46 TTTAsnLeuThHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeu 65
DB 63 TACAACTACAGCAATGCGCCAGCAACCAATGACACGAGAGACAGAAAGAGCGCTCG 122
QY 66 GluValHisGlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePhe 85
DB 123 GAGGTCCACCAATTCGGCGCGCTGTGGAGATCACTGCTACCGGAGCTCGCTTC 182
QY 86 LeuCySThMetLeuThTrpProIleCysLeuProAspTrpHisLysProLeuProProCys 105
DB 183 CTGTGCTATATGACAGCCCATCTGTTCCTGACTACACAGCGGCTACACCGCTGC 242
QY 106 ArgSerValCysGlnArgAlaGlyCysSerProLeuMetArgGlnTrpGlyPhe 125
DB 243 CGTTCCGTGTGCGAGGCGCCAGGCGCGCTGCTCCCGCTCATGCGCGAGTACGCGCTTC 302

QY 126 AlATPProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145
DB 303 GCGTGGCCGAGCGCATGAGCTGCACCGCTCCCTGTGTGGCGGCGGAGAGTT 362
QY 146 LeuCyMetAspTrpAsnArgSerGluAlaThrThrAlaProProArgProPheProAla 165
DB 363 CTGTATAGATTAATACCGAGGAGCCAGCCACACCGGCTCCCTTAAGTCTTCCCGGCG 422
QY 166 LysProThrLeuProGlyProGlyProGlyProGlyProGlyProGlyProGlyProGly 185
DB 423 AAACCTACACTCCGAGGACACACAGGCGGCGCATCTTCGGGGCGGATGCCCTCGGGA 482
QY 186 GlyPro 187
DB 483 GGCCCA 488

RESULT 2
AA481448 424 bp mRNA linear EST 08-AUG-1997
LOCUS zva5b07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:756565 3' similar to TR:G151252 G151252 TRANSMEMBRANE
RECEPTOR., mRNA sequence.

ACCESSION AA481448
VERSION AA481448.1 GI:2211000
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Merritt, M., Martin, J., Moore, B.,
Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wyllie,
T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seg primer: 41m13 fwd. EF from Amersham
High quality sequence Etop: 417.
Location/Qualifiers

FEATURES

source

1..424
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:756565"
/clone_1lb="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73P (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCGGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Patricia Bonaldi."

BASE COUNT 71 a 163 c 123 g 67 t
ORIGIN

Alignment Scores:
Pred. No.: 4.45e-53 Length: 424
Score: 754.00 Matches: 137
Percent Similarity: 97.87% Conservative: 1

/note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI; Site 2: NotI; The cDNA library was constructed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "

BASE COUNT 83 a 132 c 174 g 68 t

ALIGNMENT SCORES:

Pred. No.:	Length:	Matches:	Conservative:
Score:	584.00	104	2
Percent Similarity:	93.81%	Mismatches:	7
Best Local Similarity:	92.04%	Indels:	0
Query Match:	44.58%	Gaps:	0

US-09-847-102a-68 (1-235) x AM462410 (1-457)

QY 123 TygylpPhaAlaTrpProGluArgMetSerCyAspArgLeuProValLeuGlyArgasp 142
 DB 455 TACGGCTTGGCTGGCCGACGATGATGCGACCGCTCCGGTCTGGGCGCGAC 396
 QY 143 AlaGluValLeuCyMetSerPyrAsnArgSerGluAlaThrThrAlaProProArgPro 162
 DB 395 GCCGAGTCTCTGTCATGATTACACCCGACGAGGCCACACCGCTCCCGACGCC 336
 QY 163 PheProAlaArgProThrLeuProGlyProGlyAlaProAlaSerGlyGlyGlyCys 182
 DB 335 TTCGGCGTCAAGCCCACTCTCGGCTCGGCGGCTCGGCGGCGGAGAACGACTGC 276
 QY 183 ProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeuLysGlu 202
 DB 275 GCCGCGGGGGCCCGCTGGTGTGCAAGTCCGCGACCCCTTGGTCCATTGGAAGAG 216
 QY 203 SerHisProLeuTyTrAsnLysValAlaArgThrGlyGlnValProAsnCyAlaValProCys 222
 DB 215 TCACACCGCTTCAACAAAGGTCGCGAGCGGCGAGTACCAACTGCGCGTCCCTGC 156
 QY 223 TyrglnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 155 TACCAACCTCTTTCAGCCCCCGACGAGCGACCTTGC 117

RESULT 7

AZ475021 560 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0292116R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0292116 R, DNA sequence.

ACCESSION AZ475021 GI:10633146
 VERSION AZ475021
 KEYWORDS GSS.

SOURCE house mouse.
 ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 560)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0292 row: 1 column: 16
 Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
 High quality sequence stop: 560.
 Location/Qualifiers
 1..560
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0292116"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42mv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

106 a 173 c 163 g 118 t

ALIGNMENT SCORES:

Pred. No.:	Length:	Matches:	Conservative:
Score:	2,016.37	560	101
Percent Similarity:	567.00	Mismatches:	11
Best Local Similarity:	88.89%	Indels:	2
Query Match:	80.16%	Gaps:	1

US-09-847-102a-68 (1-235) x AZ475021 (1-560)

QY 11 SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaSer 28
 DB 181 TCGCTCTATATCCGCTTGGCGGTGTACAGGCTTACAGGCGCTGCCGCTTCCGCC 240
 QY 29 LysAlaProValCysGlnGluIleThrValProMetCysArgGlyTleGlyTyTrAsnLeu 48
 DB 241 AAGGAGCTGGCGTCCAGAGATCAGCGTGCCTTGTCCAAAGGATCGTTACAACTAC 300
 QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
 DB 301 ACTTACATGAGCCCAACAGTCAACACGACGACGAGATGAGGCGGCTTGAAGGTGCAC 360
 QY 69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
 DB 361 CAGTTTGGCGCTGTGTGAGATACAGTCTCCCGGACCTCAAGTTCTTTCTGTGAGC 420
 QY 89 MetTyThrProIleCysLeuProAspTyrHisLysProLeuProProCysArgSerVal 108
 DB 421 ATGTACAGCCCATCTGCTGAGAGATCAAGAAAGCTTGCCTTGTCTGTGTG 480
 QY 109 CysGluArgAlaValAlaGlyCysSerProLeuMetArgGlnTyrglyPheAlaTrpPro 128
 DB 481 TGTGAACCGCCCAAGCGCGCGCGCTCATGCGCCAGTACGAGGTTTGGCTTGGCT 540
 QY 129 GluArgMetSerCysAsp 134
 DB 541 GACCCATCGCTGCGAT 558

RESULT 8

BG438433

LOCUS BG438433 564 bp mRNA linear EST 10-MAY-2001
 DEFINITION p825d03.y2 Trichinella spiralis ML CMVspport Jaemer Trichinella
 RECEPTOR. ; mRNA sequence.
 ACCESSION BG438433
 VERSION BG438433.1 GI:13348081
 KEYWORDS EST.
 SOURCE Trichinella spiralis.
 ORGANISM Trichinella spiralis
 Eukaryota; Metazoa; Nematoda; Enoplia; Trichocephalida;
 Trichinellidae; Trichinella.
 REFERENCE 1 (bases 1 to 564)
 McCarter,J., Clifton,S., Chiappelli,B., Page,D., Martin,J., Wyle,T.,
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
 ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Doug Jaemer
 (djaemer@vetmed.wsu.edu) at Washington State University, Dept. of
 Veterinary Microbiology and Pathology DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 Seq primer: Sp6
 High quality sequence stop: 417.
 FEATURES
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 Location/Qualifiers
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 /dev_stage="muscle stage larvae"
 /lab_host="DH10B"
 /note="vector: pCMVspport-7.neo; Site_1: NotI; Site_2: SalI
 ; The library was constructed using mRNA isolated from
 total RNA with oligo-dT cellulose. Total RNA was generated
 from muscle larvae that were isolated from infected rats.
 Larvae were liberated by pepsin/HCl digestion, incubated
 with 1% SDS, treated with RNase and DNase to eliminate
 host nucleic acid contamination, and purified on a Percoll
 gradient. The T. spiralis isolate was obtained from
 Dickson Deepomier (Columbia University). The library was
 provided by Dr. Doug Jaemer (djaemer@vetmed.wsu.edu) and
 colleagues at Washington State University. DNA Sequencing
 by: Washington University Genome Sequencing Center St.
 Louis."
 BASE COUNT 144 a 151 c 149 g 120 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1e-34 Length: 564
 Score: 534.50 Matches: 89
 Percent Similarity: 86.78% Conservative: 16
 Best Local Similarity: 73.55% Mismatches: 15
 Query Match: 40.80% Indels: 1
 Gaps: 1
 US-09-847-102a-68 (1-235) x BG438433 (1-564)
 Oy 33 CysgngluilethvalprowetCysargelyllegllyTyAsnleuThrhismetPro 52
 Db 205 TGTGAGAGATCAGCATCCGATGTGCAAGTCGATCGCTACCAATATGATGCCC 264
 Oy 53 AenglnPheasnHlAspThrcInlAspqluAgluAgluValHlGlnPheTrpPro 72
 |||||

Db 265 AACCAATTCAACACCAACCAAGAGACCCGGCATGAGTGCACCACTTGGCCG 324
 Oy 73 LeuValGluilegInCysSerProAspLeuArgPhePheLeuCyThMetTyTrpPro 92
 Db 325 CTGGTCGAAATCAACTGTCAGTCCGATTTGGCTTTTCTCTTCAGCATATGACGCCG 384
 Oy 93 IlleCysLeuProAspTyThlslsPleuProProCysArgSerValCysGluArgAla 112
 Db 385 ATTGCATATGCGGATATTCGAAACCGTTGGCCGCTGCAGTCCGATGCGAACGGGCC 444
 Oy 113 LysAlaGlyCysSerProLeuMetArgGlnTyGlyPheAlaTTPProGluArgMetSer 132
 Db 445 AGGGCCGCTCGCGCCACGTATCGCGATGCGTTCGATGCGTTCGATGCGTTCGATGCG 504
 Oy 133 CysAspArgLeuProValleuGlyArgAspAlaGluValleuCysMetAspTyTrpArg 152
 Db 505 TGGCAGCAAGTTGCCGCTTCTTGGTTCGATGCGTTCGATGCGTTCGATGCGTTCGATGCG 561
 Oy 153 Ser 153
 Db 562 ACT 564
 RESULT 9
 LOCUS BG353236
 DEFINITION p825d03.y1 Trichinella spiralis ML CMVspport Jaemer Trichinella
 RECEPTOR. ; mRNA sequence.
 ACCESSION BG353236
 VERSION BG353236.1 GI:13181896
 KEYWORDS EST.
 SOURCE Trichinella spiralis.
 ORGANISM Trichinella spiralis
 Eukaryota; Metazoa; Nematoda; Enoplia; Trichocephalida;
 Trichinellidae; Trichinella.
 REFERENCE 1 (bases 1 to 559)
 McCarter,J., Clifton,S., Chiappelli,B., Page,D., Martin,J., Wyle,T.,
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
 ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Doug Jaemer
 (djaemer@vetmed.wsu.edu) at Washington State University, Dept. of
 Veterinary Microbiology and Pathology DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 Seq primer: Sp6
 High quality sequence stop: 463.
 FEATURES
 source
 Location/Qualifiers
 1..559
 /organism="Trichinella spiralis"
 /db_xref="taxon:6334"
 /clone_lib="Trichinella spiralis ML CMVspport Jaemer"
 /dev_stage="muscle stage larvae"
 /lab_host="DH10B"
 /note="vector: pCMVspport-7.neo; Site_1: NotI; Site_2: SalI
 ; The library was constructed using mRNA isolated from
 total RNA with oligo-dT cellulose. Total RNA was generated
 from muscle larvae that were isolated from infected rats.
 Larvae were liberated by pepsin/HCl digestion, incubated
 with 1% SDS, treated with RNase and DNase to eliminate
 host nucleic acid contamination, and purified on a Percoll
 gradient. The T. spiralis isolate was obtained from

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1 (bases 1 to 571)	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zagó, M.A., Bordin, S., Costa, F.F., Goldani, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496 (2000)	
	Contact: Simpson A.J.G.				

FEATURES	Location/Qualifiers
source	1. .571

Alignment Scores:	
Pred. No.:	4.56e-32
Score:	502.50
Percent Similarity:	88.14%
Best Local Similarity:	72.88%
Query Match:	38.36%
B:	12
Gaps:	1
Matches:	86
Mismatch:	18
Mismatches:	12
Indels:	2
Gaps:	1

US-09-847-102A-68 (1-235) x BE718107 (1-571)

QY 33 CysGlnGluIlePheValProMetCysArgGlyTleGlyTyrAsnLeuThiHmeCPro 52
|||:::|
Db 95 TGGAGAGAGTCCACATACCAATGTGTGGGGCATTTGCTCAACATACATCTCTTCCC 154
53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTyrPro 72
|||:::|
Db 155 AACGAGATGACCATCATGAGACCCGAGCGAAGCGGGCCCTGGAGGTGCACCAATTTCTGGCCC 214
QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysGlnMetTyrThrPro 92
|||:::|
Db 215 CTGTGTGAGATCAAAATGCTCGCCGAGCTCAAGTTCTTCTGTGAGCATTTACACGCC 274
QY 93 IleCysLeuProAspTyrHisIleAspProLeuProProCysArgSerValCysGluArgAla 112
|||:::|
Db 275 ATCTGCTGGAGGATTAACCAACAGCGCGTCCGCTTCCCGAGAGGTGTGAGAGAGAGCC 334
QY 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGluArgMetSer 132
|||:::|
Db 335 CGCTCGGAGATGCCACCTCATATGACAGAGTACACACTTCGATATGCCCGGAGAGAAATGCG 394

Oy	133	Cysasprrtgleu-Provalleugfiya-gaspaalagialvalleucysmetacp	149
Dd	395	TGCAGACACTTGCCCCCTTCATGTT---GACCCGACATCTGTGCATGGAA	443
RESULT 12			
LOCUS	A1958244		
DEFINITION	679 bp mRNA linear EST 07-JUN-2001		
	fdd2c05.y1 zebrafish washu mrimg est dario refio cdna clone		
	IMAGE:379704 5 similar to TR:O61091 O61091 FRIZZLED HOMOLOG 8 ; ,		
ACCESSION	mRNA sequence.		
VERSION	A1958244		
KEYWORDS	A1958244 GI:5750953		
SOURCE	EST .		
	zebrafish.		
ORGANISM	Danio rerio.		

FEATURES

BASE COUNT	147 a	191 c	182 g	156 t	3 others
ORIGIN					
Alignment Scores:					
Pred. No.:	7.4e-30	Length:	679		
Score:	477.00	Matches:	85		
Percent Similarity:	83.04%	Conservative:	8		
Best Local Similarity:	75.89%	Mismatches:	19		
Query Match:	36.41%	Indels:	0		
	9	Gaps:	0		
US-09-847-102A-68 (1-235) x AI958244 (1-679)					
OY	13	LeuLeuLeuLeuLeuLaGInLeuValGIyAGAlaAlaAlaSerLySaIaProVal	32		
Db	338	CTGTTCCTCGGCCTGCTCACTTACGCCGATGACGGATCACCGCCAAAGATCACC	397		
OY	33	CysGInGuIlleThVaIPrometCysArgGIyIIegLYTYrAsmLeuthriSmetPro	52		
Db	338	TGTCAAGAGATGCGCGTTCCGCTGTGCAGAAGCATCGTTTAATCACTCACTCATGCCC	457		
OY	53	AasnIpheasnhIASpThrGlnaspGluagIyleuGluValHisGlnheTrpPro	72		
Db	458	AACCAAGTTCAACCAAGACGAGATGAAGCCGGCTTGAGAGTGCACCAAGTTCTGGCT	517		
OY	73	LeuValGlulliegIncYSerProaspLeuargPhePheLeuCysThymetylThrPro	92		
Db	518.	CTGGGAGATTCACTGCTGCCCGATCTCAAGTTCTTGTGACGATGTACACCCCG	577		
OY	93	IleCYslauProaspTYHISlySProuleuProCYsarGserValCYsgluarGaIA	112		
Db	578	ATATCTCTGAGACTATPAAGANCCCCCTTNGCCGCTGCGAGAGCTTGCGAGAGACC	637		
OY	113	LysalaglCYsSerProleuMetargIntyrGIy	124		
Db	638	AAGCGGGCTGCGCCCGCTCATGCGGCANTACGG	673		
RESULT 13					
LOCUS	BB619404	607 bp	mRNA	linear	EST 31-AUG-2001
DEFINITION	BB619404.1 RIKEN full-length enriched, 8 days embryo Mus musculus				
ACCESSION	CDNA clone 573054E22 5', mRNA sequence.				
VERSION	BB619404				
KEYWORDS	BB619404.1 GI:15396804				
SOURCE	EST.				
ORGANISM	house mouse.				
REFERENCE	Mus musculus				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 607) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A ' , Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Koudd , M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki, ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001)				
TITLE	Contact: Yoshihide Hayashizaki				
JOURNAL	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sec.riken.go.jp, URL:http://genome.sec.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh , M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)				
COMMENT					

	Maatani,K., Fujiwara,S., Inoue,K., Togawa,Y., Irawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
	Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara, Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
	Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shingawa,A., Aizawa, K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, L72-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES	e mouse tissues.
SOURCE	Location/Qualifiers 1..607. /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="5730542E22" /cclone_1fb="RIKEN full-length enriched, 8 days embryo" /sex="mixed" /dev_stage="8 days embryo" /lab_host="DH10B" /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGACAGATCCCAAGAGCTCTTTTTCCTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length b cap-trapper. cDNA went through one round of subtraction t Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGACATTCTGAAGTTATTAATTAATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from lambda Phi C I. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT	95 a 222 c 179 g 111 t
ORIGIN	
Alignment Scores:	
Pred. No.:	1.36e-28 Length: 607
Percent Similarity:	461.00 Matches: 92
Best Local Similarity:	59.69% Conservative: 25
Query Match:	46.94% Mismatches: 57
DB:	35.19% Indels: 22
	10 Gaps: 7
US-09-047-102A-68 (1-235) x BB619404 (1-607)	
Oy	33 CyegInGluiLeThValPrOmEcYsArgtYllegIYrAnLmThNrHsMePPro 52
Db	51 TGGCACCCCATCTCCATCCCGCTGTGCACGAGCATCGCTCAACAACGACCATCATGCC 110
Oy	53 AsnGIInPhaasNHisAprThrGlnAspGluNlaGlyLeuGluValIH:sgInpHetpPro 72
Db	111 AACCTTCTTGCCACACGACGAGGAGGCGGAGCTGAGAGTGCATCGATTCTTACCG 170
Oy	73 LeuValGluileGlnCySerPrOaspLeuArpGhePheLeuCYsrHmetYrThPro 92
Db	171 CTGTGAAGTGTGAAGTGTCTCGCCGACGACTGCGCTTCTTCCGTGTCTCATATGACGCCG 230
Oy	93 IleCyLeuPrOaspLyTrHisLyseProleuPrOpProcYsarGerValCySGluarGala 112


```

Db      211 GTGTCACAGTG---CTGAGACGAGCCATCCCGCGCTGCTCCATCTGCAGAGCGCG 287
Oy      113 LysAlaGlyCySeSerProLeuMetArGIntYrGlyPheAlaTriProGluArgMetSer 132
Db      288 CGCCAGAGCTGCGAGCGCTCATGAACAAGTTCGCTTCACATGCGCGAGCGCTCCGC 347
Oy      133 CysAsePArGLeuProValLeuGlyArGAspAlaGluValLeuCyMetAspTyRAsnArg 152
Db      348 TCGGAGCATTTCCCGCTCAGCGC-----GCCGAGCAGATCTGCTGGCGCAGAACAC 401
Oy      153 SerGlu-----AlaThrThrAlaProProArgProPheProAlaLys 166
Db      402 TCGGAGACGAGCTCTGCGCTACTCAGCACCGCGCA-----CTTTTGCGCTGAG 455
Oy      167 ProThrLeuProGlyProProGlyAlaProAlaSerGlyGluCySePro-----183
Db      456 CCGCGCGCGGGGAGACCCCGCGCGCGCTGCGCGGGGAGTGGCTCGCCCGCTTACGCC 515
Oy      184 ---AlaGlyGlyProPheValCySeLysCyArGluProPheValProIleLeuLysGlu 202
Db      516 ACTGGGAGACACCTTTTCACTGTGCC-----CCGTTCTCAAGG 557
Oy      203 SerHisProLeuTyRAsnLysValArgThrGlyGlnValProAsnCyS 218
Db      558 CCG---GTTTATTTCACATATAGTTCTTGGGGGAGCGCCATGTGC 602

RESULT 14
LOCUS   AI860140 580 bp mRNA linear EST 20-DEC-1999
DEFINITION wh19f09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:383145 3'
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          sequence.
ACCESSION AI860140
VERSION   AI860140.1 GI:5513756
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 580)
          NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          CDNA Library Preparation: M. Bento Soares, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CCAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/BLN at:
          www.bio.lnlnl.gov/bbrp/image/image.html
          Insert Length: 1901 Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence scop: 460.
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              /db_xref="taxon:9606"
              /clone="IMAGE:2383145"
              /clone_11b="NCI CGAP_Kid11"
              /lab_host="MD10B"
              /note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with
              a modified polylinker; Site_1: Not I; Site_2: Eco RI;
              Plasmid DNA from the normalized library NCI CGAP Kid1 was
              prepared, and ss circles were made in vitro. Following HAP
              purification, this DNA was used as tracer in a subtractive
              hybridization reaction. The driver was PCR-amplified cDNAs
              from a pool of 5,000 clones made from the same library
              (clonoids 132376-132391, 1456007-145675, and

```

```

BASE COUNT      1500552-1502855). Subtraction by Bento Soares and M.
                  Fatima Bonaldo. "
ORIGIN          89 a 225 c 182 g 84 t
Alignment Scores:
Pred. No.:      7,04e-27 Length: 580
Score:          440.00 Matches: 88
Percent Similarity: 59.26% Conservative: 24
Best Local Similarity: 46.56% Mismatches: 55
Query Match:    33.59% Indels: 22
                  Gaps: 5
US-09-847-102a-68 (1-235) x AI860140 (1-580)
Oy      3 ArgProAspProSerAlaProProSerLeuLeuLeuLeuAlaGlnLeuValGly 22
Db      12 CGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 44
Oy      23 ArgAlaAlaAlaAlaSerLysAlaProVal--CysGlnGluIleThrValProMetCyS 42
Db      45 AGAAGGCGATCTCCATCCCGGACACGCGCTTCTGCGAGCCCATCTCCCGCTGTGCA 104
Oy      42 rGlyIleGlyTyRAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspG 62
Db      105 CGGACATCGCTTACACACAGACCATCATGCCCCAAGCTTCTGGGCGCACGACGAGAG 164
Oy      62 LuAlaGlyLeuGlnValHisGlnIleThrProLeuValGlnIleGlnIleSerProAsp 82
Db      165 AGCGAGGCTTAGAGGTGACACGATTTCTATCCGCTGGTGAAGTGCAGTGTGCGCCGAC 224
Oy      82 eUArgPhePheLeuCySerThrMetTyThrProIleCySeLeuProAspTyRHisLysProL 102
Db      225 TCGGTTCTTCTGCTGCTCCATGACGACCGCGGTGACCGTGCACCGTGCACCGTGC 281
Oy      102 eUProProCyArGSerValLysGluArgAlaLysAlaGlyCySeSerProLeuMetArG 122
Db      282 TCCCGCGCGCGCGCTTATCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 341
Oy      122 IntYrGlyPheAlaTriProGluArgMetSerCySePArGLeuProValLeuGlyArG 142
Db      342 AGTTGGTTTTCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
Oy      142 sPaLaGluValLeuCyMetAspTyRAsnAspSerGlu-----AlaT 156
Db      398 --GCCGACATATCTGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 455
Oy      156 hTrhAlaProProArgProPheProAlaLysProThrLeuProGlyProProGlyAlaP 176
Db      456 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 509
Oy      176 roAlaSerGlyGlyGluCySePro 183
Db      510 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532

RESULT 15
LOCUS   BF434722 556 bp mRNA linear EST 29-NOV-2000
DEFINITION 7p03e09.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:364457 3'
          similar to TR:O94816 O94816 FRIZZLED-7. [1], mRNA sequence.
ACCESSION BF434722
VERSION   BF434722.1 GI:11447010
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 556)
          NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.

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Yu, M.
09/1847102 Page 1
Seq ID 68 w/Inters

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 16:34:17 ; Search time 323 Seconds
(without alignments)
469.078 Million cpi1 updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARPDSPAPSLLLLLAQL.....PNCAPVCYQPSFADERTFA 235

Scoring table: BLOSUM62

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA_Main:*

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27: /cgn2_6/ptodata/1/paa/US061_COMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	235	US-09-847-102a-68	Sequence 68, Appl
2	1310	100.0	264	US-09-107-112-15	Sequence 15, Appl
3	1310	100.0	585	US-09-107-112-4	Sequence 4, Appl
4	1310	100.0	585	US-09-847-102a-51	Sequence 51, Appl
5	1310	100.0	585	US-10-146-474-9	Sequence 9, Appl
6	1310	100.0	586	US-08-832-340-10	Sequence 10, Appl

7	1310	100.0	586	US-10-152-548-10	Sequence 10, Appl
8	1310	100.0	586	US-60-015-307-10	Sequence 10, Appl
9	1306	99.7	526	US-60-207-360-270	Sequence 270, Appl
10	1306	99.7	542	US-60-229-515-752	Sequence 752, Appl
11	1311	84.8	516	US-09-847-102a-38	Sequence 38, Appl
12	1014	77.4	232	US-60-213-168-237	Sequence 237, Appl
13	1014	77.4	232	US-60-213-170-237	Sequence 237, Appl
14	920	70.2	203	US-60-177-646-3449	Sequence 3449, Ap
15	920	70.2	203	US-60-178-308-2959	Sequence 2959, Ap
16	824	62.9	277	US-09-847-102a-73	Sequence 73, Appl
17	824	62.9	694	PCT-US02-23913-144	Sequence 144, App
18	824	62.9	694	US-09-847-102a-56	Sequence 56, Appl
19	824	62.9	694	US-10-205-823-144	Sequence 144, App
20	824	62.9	694	US-60-228-045-1	Sequence 1, Appl
21	823.5	62.9	274	US-09-847-102a-74	Sequence 74, Appl
22	823.5	62.9	682	US-08-832-340-16	Sequence 16, Appl
23	823.5	62.9	682	US-10-152-548-16	Sequence 16, Appl
24	823.5	62.9	682	US-60-015-307-16	Sequence 16, Appl
25	823.5	62.9	685	US-09-107-112-10	Sequence 10, Appl
26	823.5	62.9	685	US-09-847-102a-57	Sequence 57, Appl
27	823.5	62.9	685	US-10-146-474-14	Sequence 14, Appl
28	758	57.9	137	US-60-181-425-28	Sequence 28, Appl
29	758	57.9	138	US-60-188-162-4990	Sequence 4990, Ap
30	758	57.9	138	US-60-213-844-265	Sequence 265, App
31	740.5	56.5	599	US-09-847-102a-37	Sequence 37, Appl
32	661	50.5	115	US-09-087-031-11	Sequence 11, Appl
33	661	50.5	115	US-09-087-031D-10	Sequence 10, Appl
34	621	47.4	348	US-09-107-112-16	Sequence 16, Appl
35	621	47.4	694	US-08-832-340-2	Sequence 2, Appl
36	621	47.4	694	US-09-107-112-2	Sequence 2, Appl
37	621	47.4	694	US-09-614-150-42183	Sequence 42183, A
38	621	47.4	694	US-10-152-548-2	Sequence 2, Appl
39	621	47.4	694	US-60-015-307-2	Sequence 2, Appl
40	621	47.4	694	US-60-173-386-1465	Sequence 1465, Ap
41	621	47.4	694	US-60-175-871-1645	Sequence 1645, Ap
42	621	47.4	694	US-60-184-775-1502	Sequence 1502, Ap
43	621	47.4	694	US-60-191-637-41817	Sequence 41817, A
44	621	47.4	694	US-60-191-700-1611	Sequence 1611, Ap
45	619	47.3	115	US-09-087-031E-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-847-102a-68

Sequence 68, Application US/09847102A

GENERAL INFORMATION:

APPLICANT: University of California

APPLICANT: Carson, Dennis A.

APPLICANT: Cort, Maripat

APPLICANT: Rhee, Chae-Seo

APPLICANT: Lorenzo, Leonil M.

TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

FILE REFERENCE: 22006-20629-00

CURRENT APPLICATION NUMBER: US/09/847,102A

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-09-847-102a-68

Query Match 100.0%; Score 1310; DB 22; Length 235;

Best Local Similarity 100.0%; Pred. No. 76-102;

Matches 235; Conservative 0; Mismatches 0; Indels 0;

1 MARPDSPAPSLLLLLAQLVGRRAASKAPVCQETVPCRGIGYNLTMPNPFNDTQ 60

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Db 1 MARPPSAPSLILLLLLAOLVGRAAASKAPVCOEITVPMCRGIGYNLTTHMPNDFNDTQ 60
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Db 61 DEAGLEVHGFVPLVEIQSPDLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNRSEATTAPPRFPFAKPTLPGPAPASGG 180
Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNRSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

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RESULT 2

US-09-107-112-15

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; Sequence 15, Application US/09107112
; GENERAL INFORMATION:
; APPLICANT: Kosik, Kenneth S.
; APPLICANT: Morin, Peter
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR TREATING ALZHEIMER'S DISEASE
; FILE REFERENCE: 05311/020001
; CURRENT APPLICATION NUMBER: US/09/107,112
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: US 60/051,359
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-107-112-15

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Query Match 100.0%; Score 1310; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 8e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARPPSAPSLILLLLLAOLVGRAAASKAPVCOEITVPMCRGIGYNLTTHMPNDFNDTQ 60
Qy 61 DEAGLEVHGFVPLVEIQSPDLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEVHGFVPLVEIQSPDLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNRSEATTAPPRFPFAKPTLPGPAPASGG 180
Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNRSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

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RESULT 3

US-09-107-112-4

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; Sequence 4, Application US/09107112
; GENERAL INFORMATION:
; APPLICANT: Kosik, Kenneth S.
; APPLICANT: Morin, Peter
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR TREATING ALZHEIMER'S DISEASE
; FILE REFERENCE: 05311/020001
; CURRENT APPLICATION NUMBER: US/09/107,112
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: US 60/051,359
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT

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; ORGANISM: Homo sapiens
; US-09-107-112-4

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Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DEAGLEVHGFVPLVEIQSPDLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
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Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNRSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

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RESULT 4

US-09-847-102A-51

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; Sequence 51, Application US/09847102A
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leonil M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629,00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-847-102A-51

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Query Match 100.0%; Score 1310; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNRSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPFVCKCRPEFVPIIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

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RESULT 5

US-10-146-47A-9

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; Sequence 9, Application US/1014647A
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil

```

Melkonian, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-146-474-9

Query Match 100.0%; Score 1310; DB 25; Length 585;
Best Local Similarity 100.0%; Pred. No. 2e-101;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPRFPFAKPTLLPGPPAPASGG 180
QY 181 ECPAGGPFVCKCREPVPILKESHPLYNKVRTGOVPCAVPCYOPSSADERTTA 235
DB 181 ECPAGGPFVCKCREPVPILKESHPLYNKVRTGOVPCAVPCYOPSSADERTTA 235

RESULT 6

US-08-832-340-10
Sequence 10: Application US/08832340

GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima

APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.

APPLICANT: Wang, Yanahu
APPLICANT: Hsieh, Jen-chih

APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy

APPLICANT: Nussle, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-Apr-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-Apr-1996

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hf45 protein

US-08-832-340-10

Query Match 100.0%; Score 1310; DB 12; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARDDPSAPSLILLILIAQLVGRRAAASKAPVCEITVPMCRGIGYNLTTHMNOFNHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFELCTMTPTICLPDYHKEPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFELCTMTPTICLPDYHKEPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPRFPFAKPTLLPGPPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPRFPFAKPTLLPGPPAPASGG 180
QY 181 ECPAGGPFVCKCREPVPILKESHPLYNKVRTGOVPCAVPCYOPSSADERTTA 235
DB 181 ECPAGGPFVCKCREPVPILKESHPLYNKVRTGOVPCAVPCYOPSSADERTTA 235

RESULT 7

US-10-152-548-10
Sequence 10: Application US/10152548

GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima

APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.

APPLICANT: Wang, Yanahu
APPLICANT: Hsieh, Jen-chih

APPLICANT: Andrew, Deborah

Nathans, Jeremy
Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167,30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hfz5 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-152-548-10
Query Match 100.0%; Score 1310; DB 25; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPPSAAPSLILLLLLAQLVGRAAASKAPVCOEITVPMCRGIGYNTLTHMPNFDHTQ 60
DB 1 MARPPSAAPSLILLLLLAQLVGRAAASKAPVCOEITVPMCRGIGYNTLTHMPNFDHTQ 60
QY 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPCCRVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPCCRVCERAKAGCSPLM 120
QY 121 ROYGFAMPBEMSCDRPLVGRDAEVLCDYNSSEATTAPPRPFPKPTLPGPFGAPASGG 180
DB 121 ROYGFAMPBEMSCDRPLVGRDAEVLCDYNSSEATTAPPRPFPKPTLPGPFGAPASGG 180
QY 181 ECPAGGPFVCKCRFPFVILKESHPLYNKRTGQVPCAVPCYQPSFSADERTFA 235
DB 181 ECPAGGPFVCKCRFPFVILKESHPLYNKRTGQVPCAVPCYQPSFSADERTFA 235

RESULT 8

US-60-015-307-10
Sequence 10, Application US/60015307
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
APPLICANT: Brink, Marcel

APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Hsieh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy
APPLICANT: Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/015,307
FILING DATE: 11-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hfz5 protein
US-60-015-307-10
Query Match 100.0%; Score 1310; DB 27; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPPSAAPSLILLLLLAQLVGRAAASKAPVCOEITVPMCRGIGYNTLTHMPNFDHTQ 60
DB 1 MARPPSAAPSLILLLLLAQLVGRAAASKAPVCOEITVPMCRGIGYNTLTHMPNFDHTQ 60
QY 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPCCRVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPCCRVCERAKAGCSPLM 120
QY 121 ROYGFAMPBEMSCDRPLVGRDAEVLCDYNSSEATTAPPRPFPKPTLPGPFGAPASGG 180
DB 121 ROYGFAMPBEMSCDRPLVGRDAEVLCDYNSSEATTAPPRPFPKPTLPGPFGAPASGG 180
QY 181 ECPAGGPFVCKCRFPFVILKESHPLYNKRTGQVPCAVPCYQPSFSADERTFA 235
DB 181 ECPAGGPFVCKCRFPFVILKESHPLYNKRTGQVPCAVPCYQPSFSADERTFA 235

RESULT 9

US-60-207-360-270
Sequence 270, Application US/60207360
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: RECEPTORS, AND USES THEREOF
FILE REFERENCE: CL000591

CURRENT APPLICATION NUMBER: US/60/207,360
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 386
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 270
LENGTH: 526
TYPE: PRF
ORGANISM: HUMAN
US-60-207-360-270

Query Match 99.7%; Score 1306; DB 27; Length 526;
Best Local Similarity 99.6%; Pred. No. 3.9e-101;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPDPSAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARPDPSAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCRLPVLGRDAEVLCDYNRSEATTAAPPFPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCRLPVLGRDAEVLCDYNRSEATTAAPPFPAPKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOPSFADERTFA 235
DB 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOPSFADERTFA 235

RESULT 10
US-60-229-515-752
Sequence 752, Application US/60229515
GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CL0000776
CURRENT APPLICATION NUMBER: US/60/229,515
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 2013
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 752
LENGTH: 542
TYPE: PRF
ORGANISM: HUMAN
US-60-229-515-752

Query Match 99.7%; Score 1306; DB 27; Length 542;
Best Local Similarity 99.6%; Pred. No. 4e-101;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPDPSAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARPDPSAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCRLPVLGRDAEVLCDYNRSEATTAAPPFPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCRLPVLGRDAEVLCDYNRSEATTAAPPFPAPKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOPSFADERTFA 235
DB 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOPSFADERTFA 235

RESULT 11
US-09-847-102a-38

Sequence 38, Application US/09847102A
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Corr, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leonil M.
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 516
TYPE: PRF
ORGANISM: Homo sapiens
US-09-847-102a-38

Query Match 84.8%; Score 1111; DB 22; Length 516;
Best Local Similarity 87.2%; Pred. No. 1e-84; Indels 30; Gaps 1;
Matches 205; Conservative 0; Mismatches 0;

QY 1 MARPDPSAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARPDPSAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCRLPVLGRDAEVLCDYNRSEATTAAPPFPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCRLPVLGRDAEVLCDYNRSEATTAAPPFPAPKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOPSFADERTFA 235
DB 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOPSFADERTFA 205

RESULT 12
US-60-213-169-237
Sequence 237, Application US/60213169
GENERAL INFORMATION:

APPLICANT: BEASLEY, ELLEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CL0000699
CURRENT APPLICATION NUMBER: US/60/213,169
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 678
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 237
LENGTH: 232
TYPE: PRF
ORGANISM: HUMAN
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(232)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-213-169-237

Query Match 77.4%; Score 1014; DB 27; Length 232;
Best Local Similarity 98.3%; Pred. No. 6.2e-77;
Matches 178; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 55 FNHDTDEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKA 114
DB 1 FNHDTDEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKA 60

Qy	115	GCSPLRQYGFAMPEPRMS	CDRL	PVLGRDAEVL	CDMDYNRS	SEATT	PRP	PRPAKPTL	PGPG	174
Qy	61	GCSPLVRQYGFAMPEPRMS	CDRL	PVLGRDAEVL	CDMDYNRS	SEATT	PRP	PRPAKPTL	PGPG	120
Qy	175	APASGGECPAGGAPFV	CKCRBP	FVPLIKESH	PLTNKRV	RTGVP	NCANV	PCYOPS	FSADERTF	234
Db	121	APASGGECPAGGAPFV	CKCRBP	FVPLIKESH	PLTNKRV	RTGVP	NCANV	PCYOPS	FSADERTF	180
Qy	235	A	235	A	235					
Db	181	A	181							

RESULT 13
US-60-213-170-237

Query Match	77.4%	Score 1014	DB 27	Length 232
Best Local Similarity	98.3%	Pred. No. 6.2e-77		
Matches 178; Conservative	2	Mismatches 1	Indels 0	Gaps 0

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RESULT 14
US-60-177-646-3449
; Sequence 3449, Application US/60177646
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
; FILE REFERENCE: CLO00210
; CURRENT APPLICATION NUMBER: US/60/177, 646
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 4226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3449
; LENGTH: 203
; TYPE: PRT

```

ORGANISM: HUMAN
US-60-177-646-3449

Query Match	70.2%	Score 920;	DB 27;	length 203;
Best Local Similarity	99.4%	Pred. No. 4.5e-69;		
Matches 162;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0.

```

? RESULT 15
? US-60-178-308-2959
? Sequence 2959, Application US/60178308
? GENERAL INFORMATION:
? APPLICANT: Bonazzi, Vivien
? TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
? TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
? TITLE OF INVENTION: PROTEINS, AND USES THEREOF
? FILE REFERENCE: CLO00204
? CURRENT APPLICATION NUMBER: US/60-178,308
? CURRENT FILING DATE: 2000-01-27
? NUMBER OF SEQ ID NOS: 3344
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2959
? LENGTH: 203
? TYPE: PRT
? ORGANISM: HUMAN
? US-60-178-308-2959

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Query Match	70.2%;	Score	920;	DB	27;	Length	203;
Best Local Similarity	99.4%;	Pred. No.	4.5e-69;				
Matches	162;	Conservative	1;	Mismatches	0;	Indels	0;
						Gaps	0;

Search completed: May 19, 2003, 16:41:30
Job time : 326 secs

GenCore version 5.1.4.ps.4578
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OM protein - protein search, using SW model

Run on: May 19, 2003, 16:34:42 ; Search time 90 Seconds
(without alignments)
455.046 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MAPPDPSAPSLLLLLAQL.....PNCAPCYQPSFADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 797317 seqs, 174272795 residues

Total number of hits satisfying chosen parameters: 797317

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	585	US-10-301-764-9	Sequence 9, Appl
2	1310	100.0	585	US-10-285-976-47	Sequence 47, Appl
3	1300	99.2	233	US-10-264-825-35	Sequence 35, Appl
4	824	62.9	694	US-10-311-623-6	Sequence 6, Appl
5	824	62.9	694	US-10-285-976-53	Sequence 53, Appl
6	824	62.9	694	US-10-115-678-250	Sequence 250, App
7	824	62.9	694	US-10-112-944-250	Sequence 250, App
8	824	62.9	694	US-60-452-680-21108	Sequence 21108, A
9	823.5	62.9	685	US-10-301-764-14	Sequence 14, Appl
10	818	62.4	275	US-10-264-825-38	Sequence 38, Appl
11	477	36.4	565	US-10-301-764-8	Sequence 8, Appl
12	477	36.4	565	US-10-225-557A-382	Sequence 382, App
13	477	36.4	565	US-10-285-976-41	Sequence 41, Appl
14	472.5	36.1	563	US-60-453-135-9598	Sequence 9598, Ap
15	472.5	36.1	563	US-60-453-050-9598	Sequence 9598, Ap
16	469	35.8	242	US-10-264-825-32	Sequence 32, Appl
17	461	35.2	574	US-10-285-976-51	Sequence 51, Appl
18	448	34.2	251	US-10-264-825-37	Sequence 37, Appl
19	440.5	33.6	572	US-10-301-764-13	Sequence 13, Appl
20	415	31.7	647	US-10-285-976-39	Sequence 39, Appl
21	412.5	31.5	318	US-10-264-825-31	Sequence 31, Appl
22	394.5	30.1	591	US-10-285-976-55	Sequence 55, Appl
23	393	30.0	229	US-10-264-825-39	Sequence 39, Appl
24	388	29.6	597	US-10-017-161-800	Sequence 800, App
25	384	29.3	225	US-10-264-825-40	Sequence 40, Appl
26	384	29.3	581	US-10-285-976-57	Sequence 57, Appl

27	372.5	28.4	371	US-09-949-016-7544	Sequence 7544, Ap
28	372	28.4	325	US-60-453-135-11861	Sequence 11861, A
29	372	28.4	325	US-60-453-135-11862	Sequence 11862, A
30	372	28.4	325	US-60-453-050-11861	Sequence 11861, A
31	372	28.4	325	US-60-453-050-11862	Sequence 11862, A
32	366.5	28.0	605	US-10-359-493-6297	Sequence 6297, Ap
33	366	27.9	325	US-09-610-6508-5	Sequence 5, Appl
34	345.5	26.4	368	US-09-724-676-55475	Sequence 55475, A
35	345.5	26.4	368	US-09-724-676A-55475	Sequence 55475, A
36	342.5	26.1	347	US-09-610-6508-2	Sequence 2, Appl
37	342.5	26.1	368	US-09-610-6508-4	Sequence 4, Appl
38	342.5	26.1	368	US-10-405-027-3728	Sequence 3728, Ap
39	342.5	26.1	368	US-60-452-680-12637	Sequence 12637, A
40	339.5	25.9	568	US-10-359-493-5205	Sequence 5205, Ap
41	338.5	25.8	346	PCT-US02-34777-329	Sequence 329, App
42	338.5	25.8	346	PCT-US02-37431-189	Sequence 189, App
43	338.5	25.8	346	US-10-283-017-329	Sequence 329, App
44	338.5	25.8	346	US-10-301-822-189	Sequence 189, App
45	338.5	25.8	346	US-10-126-052A-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-10-301-764-9
Sequence 9, Application US/10301764
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING APOPHOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-301-764-9
Query Match 100.0%; Score 1310; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,5e-90;
Matches 235; Conservative 0; Mismatches 0; Indels 0;

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Qy 1 MARPPSAPSLILLILLALQVGRAAAASKAPVCOEITVPMCGIGYNLTTHMNOFNHDQ 60
Db 1 MARPPSAPSLILLILLALQVGRAAAASKAPVCOEITVPMCGIGYNLTTHMNOFNHDQ 60
Qy 61 DEAGLEVHOFWFLVEIQCSPLRFFELCTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLM 120
Db 61 DEAGLEVHOFWFLVEIQCSPLRFFELCTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLM 120
Qy 121 ROYGFAMPERMSCDRLPYLGRDAEVLCDMYSSEATTAPPRFPKPTLPGPPGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPYLGRDAEVLCDMYSSEATTAPPRFPKPTLPGPPGAPASGG 180
Qy 181 ECPAGGFVCKCRPEFVPLIKESHPLYNKVRTGOVPCNCAVPCYOSFSADERTFA 235
Db 181 ECPAGGFVCKCRPEFVPLIKESHPLYNKVRTGOVPCNCAVPCYOSFSADERTFA 235
```

RESULT 2
US-10-285-976-47
Sequence 47, Application US/10285976
GENERAL INFORMATION:

APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leonil, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT FILING DATE: 2002-11-01
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 585
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzled5 (Fzd5)
US-10-285-976-47

Query Match 100.0%; Score 1310; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.5e-90;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MARPPSAPSLILLILLALQVGRAAAASKAPVCOEITVPMCGIGYNLTTHMNOFNHDQ 60
Db 1 MARPPSAPSLILLILLALQVGRAAAASKAPVCOEITVPMCGIGYNLTTHMNOFNHDQ 60
Qy 61 DEAGLEVHOFWFLVEIQCSPLRFFELCTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLM 120
Db 61 DEAGLEVHOFWFLVEIQCSPLRFFELCTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLM 120
Qy 121 ROYGFAMPERMSCDRLPYLGRDAEVLCDMYSSEATTAPPRFPKPTLPGPPGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPYLGRDAEVLCDMYSSEATTAPPRFPKPTLPGPPGAPASGG 180
Qy 181 ECPAGGFVCKCRPEFVPLIKESHPLYNKVRTGOVPCNCAVPCYOSFSADERTFA 235
Db 181 ECPAGGFVCKCRPEFVPLIKESHPLYNKVRTGOVPCNCAVPCYOSFSADERTFA 235
```

RESULT 3
US-10-264-825-35
Sequence 35, Application US/10264825
GENERAL INFORMATION:

APPLICANT: He, Biao
APPLICANT: You, Liang
APPLICANT: Xu, Zhidong
APPLICANT: Jadhon, David M.
TITLE OF INVENTION: Methods for Treating Cancer by
TITLE OF INVENTION: Inhibiting Wnt Signalling
FILE REFERENCE: 023070-125600US
CURRENT FILING DATE: US/10/264,825
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(233)
OTHER INFORMATION: human frizzled-5 peptide sequence
US-10-264-825-35

Query Match 99.2%; Score 1300; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MARPPSAPSLILLILLALQVGRAAAASKAPVCOEITVPMCGIGYNLTTHMNOFNHDQ 60
Db 1 MARPPSAPSLILLILLALQVGRAAAASKAPVCOEITVPMCGIGYNLTTHMNOFNHDQ 60
Qy 61 DEAGLEVHOFWFLVEIQCSPLRFFELCTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLM 120
Db 61 DEAGLEVHOFWFLVEIQCSPLRFFELCTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLM 120
Qy 121 ROYGFAMPERMSCDRLPYLGRDAEVLCDMYSSEATTAPPRFPKPTLPGPPGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPYLGRDAEVLCDMYSSEATTAPPRFPKPTLPGPPGAPASGG 180
Qy 181 ECPAGGFVCKCRPEFVPLIKESHPLYNKVRTGOVPCNCAVPCYOSFSADERT 233
Db 181 ECPAGGFVCKCRPEFVPLIKESHPLYNKVRTGOVPCNCAVPCYOSFSADERT 233
```

RESULT 4
US-10-311-623-6
Sequence 6, Application US/10311623
GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.; GRIFIN, Jennifer A.
APPLICANT: KALLICK, Deborah A.; TRIBOULET, Catherine M.
APPLICANT: YUE, Henry; NGUYEN, Daniel B.
APPLICANT: TANG, Y. Tom; LAL, Preeti G.
APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
APPLICANT: LU, Dying Anna M.; GRAUL, Richard C.
APPLICANT: YAO, Monique G.; BURFORD, Neil
APPLICANT: HARALIA, April J. A.; BAUGHN, Mariah R.
APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
APPLICANT: YANG, Junming; XU, Yuming
APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
APPLICANT: DUGGAN, Brendan M.; LU, Yan

TITLE OF INVENTION: RECEPTORS
FILE REFERENCE: PR-0793 USN
CURRENT APPLICATION NUMBER: US/10/311,623
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 01/19942
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/214,027
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/228,045
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/255,104
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL Program

SEQ ID NO 6
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1534444CD1
US-10-311-623-6

Query Match 62.9%; Score 824; DB 6; Length 694;
Best Local Similarity 59.9%; Pred. No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 SLL--LTLIAQLVGRAAASAKAPVCOEITVPMCRGIGYNLTMPNQFNHDTODEAGLEVH 68
DB 11 SLAALALLQSSGAAASAKELACOEITVPLCKGIGYNYTTPMQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSFDLRFPLCTMTPTICLPDYHAKPLPPCSVCERAGAGSPLMRQYGFAMP 128
DB 71 QFWPLVEIQCSFDLRFPLCSMTPTICLEDYKKPLPPCSVCERAGAGCAPLMROYGFAMP 130
QY 129 ERMSCDRLPVIGRAEAVCMQDYNRSEATTA---PPRPPAKPTLPG-----PPG 174
DB 131 DRMCDDLPEQG-NPDTLCMDYNRTDITTAAPSPRRLLPPP--PGEQPPSGSGHGRPPG 187
QY 175 A-----PASGG-----ECPAGGPFV-----CKREPFVPIIKESH 205
DB 188 ARPHRGGGSGGGGDAAPAPARGGGGKARPPGGGAAPCGQCCRAPMVSVSSERHP 247
QY 206 LYNKRTGQVNCAPVCYQPSFSADERTF 234
DB 248 LYNKRTGQIANCALPCNPFPSODERAF 276

RESULT 5

US-10-285-976-53
Sequence 53, Application US/10285976
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leonil, Lorenzo M.
APPLICANT: Corti, Mariapa
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
TITLE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
PRIOR FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzled8 (Fzd8)
US-10-285-976-53

Query Match 62.9%; Score 824; DB 6; Length 694;
Best Local Similarity 59.9%; Pred. No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 SLL--LTLIAQLVGRAAASAKAPVCOEITVPMCRGIGYNLTMPNQFNHDTODEAGLEVH 68
DB 11 SLAALALLQSSGAAASAKELACOEITVPLCKGIGYNYTTPMQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSFDLRFPLCTMTPTICLPDYHAKPLPPCSVCERAGAGSPLMRQYGFAMP 128

DB 71 QFWPLVEIQCSFDLRFPLCSMTPTICLEDYKKPLPPCSVCERAGAGCAPLMROYGFAMP 130
QY 129 ERMSCDRLPVIGRAEAVCMQDYNRSEATTA---PPRPPAKPTLPG-----PPG 174
DB 131 DRMCDDLPEQG-NPDTLCMDYNRTDITTAAPSPRRLLPPP--PGEQPPSGSGHGRPPG 187
QY 175 A-----PASGG-----ECPAGGPFV-----CKREPFVPIIKESH 205
DB 188 ARPHRGGGSGGGGDAAPAPARGGGGKARPPGGGAAPCGQCCRAPMVSVSSERHP 247
QY 206 LYNKRTGQVNCAPVCYQPSFSADERTF 234
DB 248 LYNKRTGQIANCALPCNPFPSODERAF 276

RESULT 6

US-10-115-678-250
Sequence 250, Application US/10115678
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Duntui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805ACON
CURRENT APPLICATION NUMBER: US/10/115,678
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 10/112,944
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/306,971
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: Pf_Fl_genes Version 5.0
SEQ ID NO 250
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-10-115-678-250

Query Match 62.9%; Score 824; DB 6; Length 694;
Best Local Similarity 59.9%; Pred. No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 SLL--LTLIAQLVGRAAASAKAPVCOEITVPMCRGIGYNLTMPNQFNHDTODEAGLEVH 68
DB 11 SLAALALLQSSGAAASAKELACOEITVPLCKGIGYNYTTPMQFNHDTODEAGLEVH 70

Oy	69	QFWPLVEIQGSPDLRFELCTMYTICLPDYHKNPLPCRCVCRKAKACSPMLMQYAMP	128
Dd	71	QFWPLVEIQGSPDLRFELCTMYTICLPDYHKNPLPCRCVCRKAKACSPMLMQYAMP	130
Oy	129	ERMSCDRLPVLGRDAEVLCMOYNSEATTA---PPRPAPKPTLPG-----PQG	174
Dd	131	DRMRCDRLPEEG-NBDTLCMOYNRTDLTTAAPSPRRLPRPP-PGHPQPSGCHGRPG	187
Oy	175	A-----PASGG-----ECAGGPVV---CKREPRVPILKSHS	205
Dd	188	ARPHRGGRGGGGDDAAPARGGGGGKGARPPGGGAAPCCOCRAVSVSSERRH	247
Oy	206	LYNKVRTGOVNCAVCYPQSFSADERTF	234
Dd	248	LYNRKVTCGIANCALCECHNPFESODERAF	276

RESULT 7
US-10-112-944-250

Query Match	62.9%;	Score 824;	DB 6;	Length 694;
Best Local Similarity	59.9%;	Pred. No. 5.2e-54;		
Matches 161; Conservative	21;	Mismatches 39;	Indels 48;	Gaps 8

[illegible][illegible]

```

RESULT 8
US-60-452-680-21108
; Sequence 21108, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 21108
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-21108

```

Query Match	62.9%;	Score 824;	DB 7;	Length 694;
Best Local Similarity	59.9%;	Pred. No. 5.2e-54;		
Matches 161;	Conservative 21;	Mismatches 39;	Indels 48;	Gaps 8

Qy	11	SLT	..LILL	AGVRAAAASAP	PCIOET	VTMCG	IGYNI	LTHM	NOFNH	DOBA	GEVH	68		
Db	11	SLT	..LILL	AGVRAAAASAP	PCIOET	VTMCG	IGYNI	LTHM	NOFNH	DOBA	GEVH	70		
Qy	69	QFWPLVEIQCS	PDRLRF	PLCTMYTE	ICL	PDYHK	PLP	PCRS	VCSER	KACGS	PLMROYG	FAMP	128	
Db	71	QFWPLVEIQCS	PDRLRF	PLCTMYTE	ICL	EDYK	PKP	PCRS	VCSER	KACG	APLIMROYG	FAMP	130	
Qy	129	ERMSCDRL	PVLGR	DAEVI	CM	YNS	SEATTA	---	PPRP	PAK	ETL	PG	176	
Db	131	DRMRCDRL	PEEG	-N	DTLC	MYNT	DTL	TAAP	SP	PR	RL	PPP	178	
Qy	175	A	-----	-PASG	---	EC	PAG	PFV	---	CK	RE	PVPLIK	205	
Db	188	ARPHRG	GGGGG	DDAA	APAR	GGGGG	GKAR	PPGGG	GA	CP	CG	CRAP	VS	244
Qy	206	LYNKRT	QOVN	CAVPC	Q	PS	FSD	ERF	234					
Db	248	LYNR	YKTG	IOAN	CA	LPCH	NPF	FS	OD	ER	A	276		

RESULT 9
 US-10-301-764-14
 ; Sequence 14, Application US/10301764
 ; GENERAL INFORMATION:
 ; APPLICANT: Umansky, Samuil
 ; Melkonyan, Hovsep
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; METHODS OF USE THEREOF
 ;
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ;

COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-301-764-14

Query Match 62.9%; Score 823.5; DB 6; Length 685;
Best Local Similarity 60.0%; Pred. No. 5,66-54;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
Qy 11 SIL--LLILAQLVGRGAASAKAPVCOEITVPMCRGIGVLTMPNQFNHDTODEAGLEVH 68
Db 11 SLIALALVLRSSGGAASAKELACOEITVPLCKGIGVNYTMPNQFNHDTODEAGLEVH 70
Qy 69 QFWPLVEIQCSDDLRFELCTWYTPICLPDYHKPLPRCSVCERAKAGCSPLMRQGFAMP 128
Db 71 QFWPLVEIQCSDDLRFELCSMTTPICLEDYKPLPRCSVCERAKAGCAPLMROYGFAMP 130
Qy 129 ERMSCDRLPVLGRDAVLCMDYNRESEATTA---PPRPPAKPTLPG-----PPG 174
Db 131 DRMRCDLRLPEQG-NPDTLCMDYNRTDLTTAAPSPPRLPPPP--PGEQPPSGSGHRRPG 188
Qy 175 A-----PASGEC--PAGGPFV---CKREPFVPILESHPLYNK 209
Db 189 ARPPHGGSSRSGDAAPAPRGGKARPPGGGAAPCEPGCCRAAPMVSVSSRHPLVNR 248
Qy 210 VRTGOVNCVPCYQPSFSADERTF 234
Db 249 VKTGOIANCALPCNHPFSODERAF 273

RESULT 10
US-10-264-825-38
Sequence 38, Application US/10264825
GENERAL INFORMATION:
APPLICANT: He, Biao
APPLICANT: You, Liang
APPLICANT: Xu, Zhidong
APPLICANT: Jiaibons, David M.
TITLE OF INVENTION: Methods for Treating Cancer by
Inhibiting Wnt Signalling
FILE REFERENCE: 023070-125600US
CURRENT APPLICATION NUMBER: US/10/264,825
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 275

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)---(275)
OTHER INFORMATION: human Frizzled-8 peptide sequence
US-10-264-825-38

Query Match 62.4%; Score 818; DB 6; Length 275;
Best Local Similarity 59.9%; Pred. No. 6,76-54;
Matches 160; Conservative 21; Mismatches 38; Indels 48; Gaps 8;

Qy 11 SIL--LLILAQLVGRGAASAKAPVCOEITVPMCRGIGVLTMPNQFNHDTODEAGLEVH 68
Db 11 SLIALALVLRSSGGAASAKELACOEITVPLCKGIGVNYTMPNQFNHDTODEAGLEVH 70
Qy 69 QFWPLVEIQCSDDLRFELCTWYTPICLPDYHKPLPRCSVCERAKAGCSPLMRQGFAMP 128
Db 71 QFWPLVEIQCSDDLRFELCSMTTPICLEDYKPLPRCSVCERAKAGCAPLMROYGFAMP 130
Qy 129 ERMSCDRLPVLGRDAVLCMDYNRESEATTA---PPRPPAKPTLPG-----PPG 174
Db 131 DRMRCDLRLPEQG-NPDTLCMDYNRTDLTTAAPSPPRLPPPP--PGEQPPSGSGHRRPG 187
Qy 175 A-----PASGEC--PAGGPFV---CKREPFVPILESHP 205
Db 189 ARPPHGGGGGGGDAAPAPRGGGGGKARPPGGGAAPCEPGCCRAAPMVSVSSRH 247
Qy 206 LYNKVRTGOVNCVPCYQPSFSADERTF 232
Db 248 LYNRVKTGOIANCALPCNHPFSODER 274

RESULT 11
US-10-301-764-8
Sequence 8, Application US/10301764
GENERAL INFORMATION:
APPLICANT: Melkonian, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-301-764-8

Query Match 36.4%; Score 477; DB 6; Length 565;
 Best Local Similarity 41.9%; Pred. No. 4,8e-28;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RDPSPAPSLILLILLLAQLVGRRAAASKAPV-----COEITVPMCGIGYNLTMPNOF 55
 DB 2 RRSALPRLILLPLLLPAAGPAQFHGEKGISIPDHGFCOPISIPCTDIAYNOTIMPILL 61
 QY 56 NHDTODEAGLEVHQFWPLVEIQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 115
 DB 62 GHTNODAGLEVHQFWPLVKVQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 120
 QY 116 CSPLMKQYGFAMPERMSCDRLPVLGRDAEVLCDYNRSE-----ATTAPRRFPFA-KPT 168
 DB 121 CEALMKNKFGFWPERLRCHEHFRHG--AEQICVGQNHSEBDGAPALLTTAP--PGLQPG 175
 QY 169 LGPPGAPASGGECPAGG---PFVCKCREPVPILKESHPLYNKVRGTQGVNCAVPCVQ 224
 DB 176 AGTTPGGGPGGAPPRYATLEHFFHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226
 QY 225 PS-----FSADERTFA 235
 DB 227 PARPDGSMFFSQEETRFA 244

RESULT 12
 US-10-225-567A-382

Sequence 382, Application US/10225567A

GENERAL INFORMATION:
 APPLICANT: Lifespan Biosciences
 APPLICANT: Brown, Joseph P.
 APPLICANT: Burner, Glenna C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 382
 LENGTH: 565
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225-567A-382

Query Match 36.4%; Score 477; DB 6; Length 565;
 Best Local Similarity 41.9%; Pred. No. 4,8e-28;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RDPSPAPSLILLILLLAQLVGRRAAASKAPV-----COEITVPMCGIGYNLTMPNOF 55
 DB 2 RRSALPRLILLPLLLPAAGPAQFHGEKGISIPDHGFCOPISIPCTDIAYNOTIMPILL 61
 QY 56 NHDTODEAGLEVHQFWPLVEIQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 115
 DB 62 GHTNODAGLEVHQFWPLVKVQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 120
 QY 116 CSPLMKQYGFAMPERMSCDRLPVLGRDAEVLCDYNRSE-----ATTAPRRFPFA-KPT 168
 DB 121 CEALMKNKFGFWPERLRCHEHFRHG--AEQICVGQNHSEBDGAPALLTTAP--PGLQPG 175
 QY 169 LGPPGAPASGGECPAGG---PFVCKCREPVPILKESHPLYNKVRGTQGVNCAVPCVQ 224
 DB 176 AGTTPGGGPGGAPPRYATLEHFFHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226

QY 225 PS-----FSADERTFA 235
 DB 227 PARPDGSMFFSQEETRFA 244

RESULT 13
 US-10-285-976-41

Sequence 41, Application US/10285976

GENERAL INFORMATION:
 APPLICANT: Rhee, Chae-Seo
 APPLICANT: Malini, Sen
 APPLICANT: Wu, Christina
 APPLICANT: Leonil, Lorenzo M.
 APPLICANT: Corr, Maripat
 APPLICANT: Carson, Dennis A.
 TITLE OF INVENTION: The Regents of the University of California
 TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
 FILE REFERENCE: 023070-130320US
 CURRENT FILING DATE: 2002-11-01
 PRIOR APPLICATION NUMBER: US/10/285,976
 CURRENT FILING DATE: 2001-05-01
 PRIOR APPLICATION NUMBER: US 60/287,995
 PRIOR FILING DATE: 2001-05-01
 PRIOR APPLICATION NUMBER: WO PCT/US02/13802
 PRIOR FILING DATE: 2002-05-01
 NUMBER OF SEQ ID NOS: 232
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 41
 LENGTH: 565
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human frizzled2 (Fzd2)
 US-10-285-976-41

Query Match 36.4%; Score 477; DB 6; Length 565;
 Best Local Similarity 41.9%; Pred. No. 4,8e-28;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RDPSPAPSLILLILLLAQLVGRRAAASKAPV-----COEITVPMCGIGYNLTMPNOF 55
 DB 2 RRSALPRLILLPLLLPAAGPAQFHGEKGISIPDHGFCOPISIPCTDIAYNOTIMPILL 61
 QY 56 NHDTODEAGLEVHQFWPLVEIQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 115
 DB 62 GHTNODAGLEVHQFWPLVKVQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 120
 QY 116 CSPLMKQYGFAMPERMSCDRLPVLGRDAEVLCDYNRSE-----ATTAPRRFPFA-KPT 168
 DB 121 CEALMKNKFGFWPERLRCHEHFRHG--AEQICVGQNHSEBDGAPALLTTAP--PGLQPG 175
 QY 169 LGPPGAPASGGECPAGG---PFVCKCREPVPILKESHPLYNKVRGTQGVNCAVPCVQ 224
 DB 176 AGTTPGGGPGGAPPRYATLEHFFHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226
 QY 225 PS-----FSADERTFA 235
 DB 227 PARPDGSMFFSQEETRFA 244

RESULT 14
 US-60-453-135-9598

Sequence 9598, Application US/60453135

GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele
 APPLICANT: TAKUBOVA, Olga
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001456
 CURRENT APPLICATION NUMBER: US/60/453,135
 CURRENT FILING DATE: 2003-03-10
 NUMBER OF SEQ ID NOS: 82762
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9598
LENGTH: 563
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-135-9598

Query Match 36.1%; Score 472.5; DB 7; Length 563;
Best Local Similarity 42.7%; Pred. No. 1.1e-27;
Matches 109; Conservative 30; Mismatches 75; Indels 41; Gaps 12;

QY 7 SAPSLLL-LLLAQLVGRRAAASKAPV-----COEITVPMCRGIGYNLTMPNQFNHD 58
DB 3 SALPRLLLPLLLPAAQPAQHFGEKGISIPDHGFCOPISIPCTDIAYNQTIMPNLGH 62
QY 59 TODEAGLEVHQFWPVLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCRAXACSP 118
DB 63 NOEDAGLEVHQFWPVLVKQCSPELRFLLCSMYAPVCTV-LEQAIPPCRSICERAROGCEA 121
QY 119 LMRQYGFAPWERMSCDRLVLCGRDAEVLCDYNRSE-----ATTAPRRPFA-KPTLPG 171
DB 122 LMNKGFGQWPERLRCEHFRHG--AEQICVGQNHSEGDAPALLTTAP--PGLQPGAG 176
QY 172 PRGAPASGGECPAGG---PFVCKCREPFVPIKESHPLYNKVRGTQVNCAPVCYOPS- 226
DB 177 TFGGPGGGAPPRVATLEHFRHCP-----RVLKV--PSYLSYKFLGERDCAAPC-EPAR 227
QY 227 -----FSADERTFA 235
DB 228 PDGSMFFSQEETRFA 242

RESULT 15
US-60-453-050-9598
Sequence 9598. Application us/60453050
GENERAL INFORMATION:
APPLICANT: CARCILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9598
LENGTH: 563
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-050-9598

Query Match 36.1%; Score 472.5; DB 7; Length 563;
Best Local Similarity 42.7%; Pred. No. 1.1e-27;
Matches 109; Conservative 30; Mismatches 75; Indels 41; Gaps 12;

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DB 3 SALPRLLLPLLLPAAQPAQHFGEKGISIPDHGFCOPISIPCTDIAYNQTIMPNLGH 62
QY 59 TODEAGLEVHQFWPVLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCRAXACSP 118
DB 63 NOEDAGLEVHQFWPVLVKQCSPELRFLLCSMYAPVCTV-LEQAIPPCRSICERAROGCEA 121
QY 119 LMRQYGFAPWERMSCDRLVLCGRDAEVLCDYNRSE-----ATTAPRRPFA-KPTLPG 171
DB 122 LMNKGFGQWPERLRCEHFRHG--AEQICVGQNHSEGDAPALLTTAP--PGLQPGAG 176
QY 172 PRGAPASGGECPAGG---PFVCKCREPFVPIKESHPLYNKVRGTQVNCAPVCYOPS- 226
DB 177 TFGGPGGGAPPRVATLEHFRHCP-----RVLKV--PSYLSYKFLGERDCAAPC-EPAR 227
QY 227 -----FSADERTFA 235
DB 228 PDGSMFFSQEETRFA 242

Search completed: May 19, 2003, 16:43:09
Job time : 94 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 21:14:04 ; Search time 2410 Seconds
(without alignments)
2451.653 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARDPSPAPSLILLALLAQL.....PNCAPVCYQPSFADERTFA 235

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Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
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2	1310	100.0	2334	14	US-09-053-375B-1495
3	1310	100.0	2334	15	US-09-107-112-3
4	1310	100.0	2334	41	US-10-152-548-9
5	1310	100.0	2334	45	US-60-015-307-9
6	1306	99.7	3124	64	US-60-207-360-77

QY 201 LysGUSerHsPLeuTyRAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
DB 921 AAGAGTACACACCCCTCTACACAAAGGTGCGAGCGGCGAGTGCACCACTGCGCGGTA 980
QY 221 ProCyTYRgInProSerPheSerAlaAspGluArgThrPheAla 235
DB 981 CCTCTACTACAGCCGCTCTTCAGTGCAGCGAGCGACGTTGCGC 1025

RESULT 2
US-09-053-375B-1495
; Sequence 1495, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilaehvilli, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1495
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-1495

Alignment Scores:
Pred. No.: 2, 01e-73 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-847-102a-68 (1-235) x US-09-053-375B-1495 (1-2334)

QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
DB 321 ATGGCTCGGCGCTGACCACTGACGACATGCGCGGCGCTGCTGCTGCTGCGGAGCTG 380
QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluIleThrValProMet 40
DB 381 GTGGGCGGGGCGGCGCGCGCTGCAAGGCGCGGTGTGTCAGAAATCAACGCGGCCATG 440
QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
DB 441 TCCCGGGGATGGCTACCACTGACGACATGCGCGGCGCTGCTGCTGCTGCGGAGCTG 500
QY 61 AspGluAlaGlyLeuGlnValHisGlnPheTyrProLeuValGluIleGlnCysSerPro 80
DB 501 GACGAGGCGGCGCTGAGAGTGCACCACTTCTGCGCGCTGAGATTCAAATGCTGCGCG 560
QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
DB 561 GACCTGCGCTTCTCTATGCACTATGTAACGCGCATCTGTCTGCCAGTACCAACAG 620
QY 101 ProLeuProProCysArgSerValCysGlnArgAlaLysAlaGlyCysSerProLeuMet 120
DB 621 CCGCTGCGCGCTGCGCTGCGTGTGTCGAGCGGCGGCGGCGGCTGCTGCGCGCTGAG 680
QY 121 ArgGlnTyrGlyPheAlaTyrProGluArgMetSerCysAspArgLeuProValLeuGly 140
DB 681 CCGCAGTACGCTTCTGCTGCGCGCGCGCGCATGAGTGTGACCGCTCCCGGTGCTGGG 740
QY 141 ArgAspAlaGlyValLeuCysMetAspTyrAsnArgSerGlnAlaThrThraAlaProPro 160
DB 741 CCGCAGCGCGAGGTCTCTGCACTGATTAACCGGACGAGGCGCACACGCGGCGCGCG 800
QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaAlaProLysArgGly 180
DB 801 AGGCTTTCCAGCCCAAGCCACCTTCCAGGCGCGCGCGGCGCGCTGCGGCGGCG 860

QY 181 GluCyProAlaGlyGlyProPheValCysLysGluProPheValProIleLeu 200
DB 861 GAATGCCCCCGCTGGGGCGCGCTTGTGTGCAAGTGTCCGAGCCCTTGTGCGCATTTG 920
QY 201 LysGUSerHsPLeuTyRAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
DB 921 AAGAGTACACACCCCTCTACACAAAGGTGCGAGCGGCGAGTGCACCACTGCGCGGTA 980
QY 221 ProCyTYRgInProSerPheSerAlaAspGluArgThrPheAla 235
DB 981 CCTCTACTACAGCCGCTCTTCAGTGCAGCGAGCGACGTTGCGC 1025

RESULT 3
US-09-107-112-3
; Sequence 3, Application US/09107112
; GENERAL INFORMATION:
; APPLICANT: Kosik, Kenneth S.
; APPLICANT: Morin, Peter
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR TREATING ALZHEIMER'S DISEASE
; FILE REFERENCE: 05311/020001
; CURRENT APPLICATION NUMBER: US/09/107,112
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: US 60/051,359
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (321)...(2075)
US-09-107-112-3

Alignment Scores:
Pred. No.: 2, 01e-73 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-847-102a-68 (1-235) x US-09-107-112-3 (1-2334)

QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
DB 321 ATGGCTCGGCGCTGACCACTGACGACATGCGCGGCGCTGCTGCTGCTGCGGAGCTG 380
QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluIleThrValProMet 40
DB 381 GTGGGCGGGGCGGCGCGCGCTGCAAGGCGCGGTGTGTCAGAAATCAACGCGGCCATG 440
QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
DB 441 TCCCGGGGATGGCTACCACTGACGACATGCGCGGCGCTGCTGCTGCTGCGGAGCTG 500
QY 61 AspGluAlaGlyLeuGlnValHisGlnPheTyrProLeuValGluIleGlnCysSerPro 80
DB 501 GACGAGGCGGCGCTGAGAGTGCACCACTTCTGCGCGGTGTGAGATTCAAATGCTGCGCG 560
QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
DB 561 GACCTGCGCTTCTCTATGCACTATGTAACGCGCATCTGTCTGCCAGTACCAACAG 620
QY 101 ProLeuProProCysArgSerValCysGlnArgAlaLysAlaGlyCysSerProLeuMet 120
DB 621 CCGCTGCGCGCTGCGCTGCGTGTGTCGAGCGGCGGCGGCGGCTGCTGCGCGCTGAG 680
QY 121 ArgGlnTyrGlyPheAlaTyrProGluArgMetSerCysAspArgLeuProValLeuGly 140
DB 681 CCGCAGTACGCTTCTGCTGCGCGCGCGCGCATGAGTGTGACCGCTCCCGGTGCTGGG 740

QY 141 ArgaspAlaGluValIleuCySmetAspTYRAsnArgSerGluAlaThrThrAlaProPro 160
 DB 741 CCGGAGCGCGAGGTCTCTGATGATTAACAACCGAGCGAGCGACACCGGGCCCCC 800
 QY 161 ArgProPheProAlaIysProThrIleuProGlyProProGlyAlaProAlaSerGlyGly 180
 DB 801 AGGCTTTCCAGCCAGCCACCCCTTCCAGGCGCCGCGGGGGCGGCGCTCGGGGGGC 860
 QY 181 GluCySProAlaGlyIleProPheValCysIysCyArgGluProPheValProIleLeu 200
 DB 861 GAATGCCCGCGTGGGGGCGGCTTCTGTCGACAGTGTCCGAGCGCTTCTGCGCCATTCTG 920
 QY 201 LysGluSerHisProLeuTyrAsnIysValArgThrGlyGlnValProAsnCysAlaVal 220
 DB 921 AAGAGTCAACACCCGCTTACAACAAGTGGCGAGCGGCGAGTGCCTCCAACTCGCGGT 980
 QY 221 ProGlyTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 981 CCTGCTACAGCGCGTCTTCACTGCGCAGAGCGACGCTTCCGC 1025

RESULT 4

US-10-152-548-9
 Sequence 9, Application US/10152548

GENERAL INFORMATION:

APPLICANT: Bhanot, Purnima

Brink, Marcel

Harryman, Cindy S.

Wang, Yanshu

Hsieh, Jen-chih

Andrew, Deborah

Nathans, Jeremy

Nusse, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/152,548

FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/832,340

FILING DATE: 11-APR-1997

APPLICATION NUMBER: US 60/015,307

FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8600-0167.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2334 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Human transmembrane receptor

SEQUENCE DESCRIPTION: SEQ ID NO: 9: (Friezzled 5) mRNA, Coding region: 321..2078

US-10-152-548-9

Alignment Scores:

Pred. No.: 2,01e-73

Percent: 1310.00

Score Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 41

Gaps: 0

US-09-847-102a-68 (1-235) x US-10-152-548-9 (1-2334)

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DB 321 ATGGCTCGGCTGAGCCATCCGCGCGCTTGGCTGTCTGCTCTGCGGAGCTG 380

QY 21 ValGlyArgAlaAlaAlaAlaSerIysAlaProValCysGlnGluIleThrValProMet 40

DB 381 GTGGCGCGGCGCGCGCGCGCTCAAGGCGCGGTGTGCGAAGAAATCAGGTCGCCATG 440

QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60

DB 441 TCCCGCGCGATCGCTTACCACTGACGACATGCCACCACTTCAACACGACACGACG 500

QY 61 AspGluAlaGlyLeuGluValHisGlnPheThrProLeuValGluIleGlnCysSerPro 80

DB 501 GACGAGCGCGGCGCTGAGGTGACCACTTCCGCGCTGTGGAGATCAATGCTCGCGG 560

QY 81 AspleuArgPhePheLeuCySThrMetCysThrThrProIleCysLeuProAspTyrHisIlys 100

DB 561 GACCTGCGCTTCTTCACTGACATGTAACAGCCCATCTGCTGCCACTACACCAAG 620

QY 101 ProLeuProProCysArgSerValCysGluArgAlaIysAlaGlyCysSerProLeuMet 120

DB 621 CCGCTGCGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680

QY 121 ArgGlnTyrGlyPheAlaThrProGluArgMetSerCysAspArgLeuProValIleuGly 140

DB 681 CCGCAGTACGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740

QY 141 ArgaspAlaGluValIleuCySmetAspTYRAsnArgSerGluAlaThrThrAlaProPro 160

DB 741 CCGGAGCGCGAGGTCTCTGATGATTAACAACCGAGCGAGCGACACCGGGCCCCC 800

QY 161 ArgProPheProAlaIysProThrIleuProGlyProProGlyAlaProAlaSerGlyGly 180

DB 801 AGGCTTTCCAGCCAGCCACCCCTTCCAGGCGCCGCGGGCGGCGCTCGGGGGGC 860

QY 181 GluCySProAlaGlyIleProPheValCysIysCyArgGluProPheValProIleLeu 200

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QY 221 ProGlyTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235

DB 981 CCTGCTACAGCGCGTCTTCACTGCGCAGAGCGACGCTTCCGC 1025

RESULT 5

US-60-015-307-9

Sequence 9, Application US/60015307

GENERAL INFORMATION:

APPLICANT: Bhanot, Purnima

APPLICANT: Brink, Marcel

APPLICANT: Harryman, Cindy S.

APPLICANT: Wang, Yanshu

APPLICANT: Hsieh, Jen-chih

APPLICANT: Andrew, Deborah

APPLICANT: Nathans, Jeremy

APPLICANT: Nuss, Roel
 TITLE OF INVENTION: Wnt Receptor Compositions and Methods
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/015,307
 FILING DATE: 11-APR-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0980
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2334 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human transmembrane receptor
 INDIVIDUAL ISOLATE: (frizzled 5) mRNA, Coding region: 321..2078
 US-60-015-307-9

Alignment Scores:
 Pred. No.: 2,016-73 Length: 2334
 Score: 1310.00 Matches: 235
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 45 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-015-307-9 (1-2334)
 QY 1 MetalaatgProaspProseralaproProserleuLeuLeuLeuLeuLeuLeu 20
 DB 321 ATGGCTCGGCGCCGACCACTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 380
 QY 21 ValGlyArgAlaAlaAlaAlaSerlyAlaProValCysGlnGlnIleThrValProMet 40
 DB 381 GTGGGCGGGGCGCGCGCGCGCTCAAGGCGCGGTGTGCGCAAGATCAACGAGTGC 440
 QY 41 CysAargGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 441 TCCCGCGGCGATCGGCTACCACTGACGACGACGACGCCAACAATTCAACACACACG 500
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheThrProLeuValGlnIleGlnCysSerPro 80
 DB 501 GACGAGGCGGCGCTGAGAGTGCACCACTTCTGCGCGCTGTGAGATTCACATGCTGCG 560
 QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisIlys 100
 DB 561 GACGCGCGCTTCTCTATGACATATGACACGCGCATCTGTGCGCGAGTACACCAAG 620
 QY 101 ProLeuProProCysArgSerValCysGluArgAlaValAlaGlyCysSerProLeuMet 120
 DB 621 CCGTGGCGCGCTGCGCTGCTGTGTGTGCGAGCGCCAGCGCGGCTGCTGCGCGTGA 680

QY 121 ArgGlnTyrGlyPheAlaIleTyrProGluArgMetSerCysAspArgLeuProValLeuGly 140
 DB 681 CGCCAGTACGCGCTTCTGCTGCGCGCGAGGCGATGAGCTGCGACCGCTCCGAGTGTGG 740
 QY 141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 DB 741 CGCGAGCGCGAGGTCTCTGATGATATACACCGACGAGGCGACCAACGCGCGCGCC 800
 QY 161 ArgProPheProAlaValProThrLeuProGlyProProGlyAlaProAlaSerGlyI 180
 DB 801 AGCGCTTCCAGACGACCAACCACTTCCAGCGCGCGCGCGCGCGCGCGCGCGCG 860
 QY 181 GluCysProAlaGlyGlyProPheValCysIysCysArgGluProPheValProIleLeu 200
 DB 861 GAATGCCCGCGCTGGGGCGCGCTTCTGCTGCAAGTGTCCGAGCGCTTCTGCTGCTG 920
 QY 201 LysGluSerHisProLeuTyrAsnIleValArgThrGlyGlnValProAspCysAlaVal 220
 DB 921 AAGAGTACACCGCGCTTACACAGAGTGGAGCGGCGCGAGTCCCAACTGCGCGGTA 980
 QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 981 CCTGCTACAGCGCTCTTCAAGTCCGACGAGCGCGACCTTCCG 1025

RESULT 6
 US-60-207-360-77
 Sequence 77, Application US/60207360
 GENERAL INFORMATION:
 APPLICANT: Beasley, Ellen
 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
 TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 FILE REFERENCE: C0000591
 CURRENT APPLICATION NUMBER: US/60/207,360
 CURRENT FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 386
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 77
 LENGTH: 3124
 TYPE: DNA
 ORGANISM: HUMAN
 US-60-207-360-77

Alignment Scores:
 Pred. No.: 4,856-73 Length: 3124
 Score: 1306.00 Matches: 234
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.57% Mismatches: 0
 Query Match: 99.69% Indels: 0
 DB: 64 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-207-360-77 (1-3124)
 QY 1 MetalaatgProaspProseralaproProserleuLeuLeuLeuLeuLeuLeu 20
 DB 547 ATGGCTCGGCGCTGACCACTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 606
 QY 21 ValGlyArgAlaAlaAlaAlaSerlyAlaProValCysGlnGlnIleThrValProMet 40
 DB 607 GTGGGCGGGGCGCGCGCGCGCTCAAGGCGCGGTGTGCGCAAGATCAACGAGTGC 666
 QY 41 CysAargGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 667 TCCCGCGGCGATCGGCTACCACTGACGACATGCCCAACAGTTCAACACACACGAG 726
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheThrProLeuValGlnIleGlnCysSerPro 80
 DB 727 GACGAGGCGGCGCTGAGAGTGCACCACTTCTGCGCGCTGTGAGATTCACATGCTGCG 786
 QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisIlys 100
 DB 787 GACGCGCGCTTCTCTATGACATATGACACGCGCATCTGTGCGCGAGTACACCAAG 846

QY 101 ProleuProProCysArgSerValCysGluValAlaGlyCysSerProleuMet 120
 DB 847 CCGCTCCGCGCCGCTCGGTGCGAGCGCGCCAGCGCGCTGCTCGCGCTGATG 906
 QY 121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
 DB 907 CGCGATTACGGCTTCCTCGGTGCGAGCGCGATGAGCTGGACCGCTCCGGTCTGGG 966
 QY 141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 DB 967 CGGAGCGCGAGGTCTCTGATGATGATTCACACCGAGAGGCGCACACGCGCGCCCC 1026
 QY 161 ArgProPheProAlaAlaSerProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180
 DB 1027 AGGCGCTTCCCGACGCGCAAGCCCACTTCAGAGCGCGCGCGCGCGCGCGCGCGG 1086
 QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProleu 200
 DB 1087 GAATGCCCGCTGGGGGCGCGGTTCGTGTCAGTGTGCGAGCGCTTCGCTGCTGCTG 1146
 QY 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
 DB 1147 AAGGATCACAACCGCTCTACACAGTGGCGAGCGCGCGCGCGCGCGCGCGCGGTA 1206
 QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 1207 CCTGCTACAGCGCTCTCTCAGTGCAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1251

RESULT 7

US-60-129-391-1913
 ; Sequence 1913, Application US/60129391
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith et al.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN THE DIAGNOSIS AND TREATMENT C
 ; FILE REFERENCE: 107196, 138
 ; CURRENT APPLICATION NUMBER: US/60/129,391
 ; NUMBER OF SEQ ID NOS: 1999-04-13
 ; SEQ ID NO 1913
 ; LENGTH: 2555
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1), (2552), (2553), (2554), (2555)
 ; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
 US-60-129-391-1913

Alignment Scores:

Pred. No.: 6,13e-71 Length: 2555
 Score: 1271.50 Matches: 232
 Percent Similarity: 99.15% Conservative: 1
 Best Local Similarity: 98.72% Mismatches: 1
 Query Match: 97.06% Indels: 2
 DB: 56 Gaps: 1

US-09-847-102a-68 (1-235) x US-60-129-391-1913 (1-2555)

QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuLeuLeuLeu 20
 DB 383 ATGGCTCGGCTGACCATTCGCGCGCGCTTCGCTGCTGCTGCTGCGCGAGCTG 442
 QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValPromet 40
 DB 443 GTGGCGCGGAGCGCGCGCGGTCCAGGC-CCG---TGCCAGGAATTCACGGTGGCCATG 498
 QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 499 TGCCTGGGATGGCTACCAACCTGACGACATGCCCAACAGTTCAACACGACGACGAG 558
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80

DB 559 GACGAGCGGCGCTGAGAGTGCACCATTCGCGCGCTGCGAGATCCATGCTCGCGC 618
 QY 81 AspleuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
 DB 619 GACCTGGCGCTTCTCTATGCTCTATGCTATACAGGCCCATCTGCTCCGAGTACCAAG 678
 QY 101 ProleuProProCysArgSerValCysGluValAlaGlyCysSerProleuMet 120
 DB 679 CGGCTCGCGCGCTGCGCTCGGTGCGAGCGCGCGCAAGCGCGCGCTGCTGCGCTGATG 738
 QY 121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
 DB 739 CGCGATTACGGCTTCCTGCTGCGCGCGCGCGCATGAGCTCGACCGCTCCGGTCTGGG 798
 QY 141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 DB 799 CGCGAGCGCGAGTCTCTGATGATTCACACCGCAGGAGGCGCACACGCGCGCCCC 858
 QY 161 ArgProPheProAlaAlaSerProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180
 DB 859 AGGCGCTTCCCGACGCGCAAGCCCACTTCAGAGCGCGCGCGCGCGCGCGCGCGG 918
 QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProleu 200
 DB 919 GAATGCCCGCTGGGGGCGCGGTTCGTGTCAGTGTGCGAGCGCTTCGCTGCTGCTG 978
 QY 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
 DB 979 AAGGATCACAACCGCTCTACACAGTGGCGAGCGCGCGCGCGCGCGCGCGCGGTA 1038
 QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 1039 CCTGCTACAGCGCTCTCTCAGTGCAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1083

RESULT 8

US-60-360-207-18143
 ; Sequence 18143, Application US/60360207
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321
 ; CURRENT APPLICATION NUMBER: US/60/360,207
 ; NUMBER OF SEQ ID NOS: 2002-03-01
 ; SEQ ID NO 18143
 ; LENGTH: 1758
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-60-360-207-18143

Alignment Scores:

Pred. No.: 9,73e-70 Length: 1758
 Score: 1250.00 Matches: 224
 Percent Similarity: 97.02% Conservative: 4
 Best Local Similarity: 95.32% Mismatches: 7
 Query Match: 95.42% Indels: 0
 DB: 80 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-360-207-18143 (1-1758)

QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuLeuLeuLeu 20
 DB 1 ATGGCTCGACCGGACCGCTGCGCGCTCTCTCTCTGCTGCTGCTGCTGCGCGAGCTG 60
 QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValPromet 40
 DB 61 GTGGCGCGGAGCGCGCGCGCTCCAGGCGCGCGGTGCCAGGAATACAGGTGGCCATG 120
 QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 121 TCCGAGGATGGCTTACCACTGACGACATGCCCAACCACTTACCACTACACGAG 180
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80

Db 181 GACGAGGAGGCTGAGAGTGCACCAATTCGGCGCTTGAGATATCAGCTCACC 240
Qy AspleuAcphePheLeuCyethrmetTyrThrProileCysLeuProaspTyrhis 100
Db 241 GACGCGCCCTTCTCTGTCTGTATGACAGCCCATCTGTTGCTGACATCACAAG 300
Qy 101 ProleuProProCyAargserValCysgluAargValaValaValaCysSerProleuMet 120
Db 301 CCGCTACACACCGGCGCTTCGCTGCGAGCGCCCAAGCGCGGCTGCTCGCCGCTCATG 360
Qy 121 ArgGlnTyrGlyPheAlaTyrProGluAargMetSerCysAspArgLeuProValleuGly 140
Db 361 CGCAGTACGCGCTTCTGTGCGCCGAGCGCAAGACTGCGACCGCTCTGCTGTGAGC 420
Qy 141 ArgAspAlaGluValleuCysMetAspTyrAsnaArgserGluAlaThrThrAlaProPro 160
Db 421 GCGGAGCGCGAGGCTTCTGTGTATGATTAACCAAGCAAGCAACACCGCGCTCCT 480
Qy 161 ArgProPheProAlaLysProThrleuProGlyProProGlyAlaProAlaSerGlyGly 180
Db 481 AAGTCTTCCGCGCAAACTTACCTCCAGGACCAACGAGGCGCCCATCTTCGCGGAGC 540
Qy 181 GluCyProAlaGlyGlyProPheValCysLysCysArgGluProPheValProileu 200
Db 541 GAGTCCCTCGGAGGCGCCATCCGTGTGACAGTCCGCGACCTTGTGCTCCATCTCTG 600
Qy 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
Db 601 AAGGAGTACACCCACTTACACAAAGGTGCGACCGCGCAAGTCCCACTGCGCGGTG 660
Qy 221 ProCyTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
Db 661 CCTCTACACAGCCGCTTCTGAGCCGAGCGAGCGCACTTGCC 705

RESULT 9

US-60-229-515-1423
; Sequence 1423, Application US/60229515
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000776
; CURRENT APPLICATION NUMBER: US/60/229,515
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1423
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-515-1423

Alignment Scores:

Pred. No.: 5,4e-68 Length: 1630
Score: 1222.00 Matches: 217
Percent Similarity: 100.00% Conservatve: 1
Best Local Similarity: 99.54% Mismatches: 0
Query Match: 93.28% Indels: 0
DB: 66 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-229-515-1423 (1-1630)

Qy 18 AlaGlnLeuValGlyArgAlaAlaAlaSerLysAlaProValCysGlnGluLeuThr 37
Db 3 GCGCAGCTGCTGCGCGCGCGCGCGCGCGCTCAAGCGCGCTGTCAGGAAATCAAG 62
Qy 38 ValPrometCysArgGlyLysGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHis 57
Db 63 GTGCCCACTGTGCGCGCGCATCGGCTACAACTCGAAGCATATCCCAACAGTTCAACAC 122
Qy 58 AspThrGlnAspGluAlaGlyLeuGlnValHisGlnPheThrProLeuValGlnIleGln 77

Db 123 GACAGCGAGAGCGAGCGGCGCTGAGGTGCACCAAGTTCGCGCTGTGAGATCCAA 182
Qy 78 CysSerProAspLeuArgPhePheLeuCyethrmetTyrThrProileCysLeuProAsp 97
Db 183 TGTCTGCGGAGCTGCGCTTCTTCTATGCTATGACAGCCCATCTGTCTGTGCGGAC 242
Qy 98 TyrHisLysProLeuProProCyAargserValCysgluAargValaValaValaCysSer 117
Db 243 TACCAAGAGCGCTGCGCGCTTCGCTGCGAGCGCGCCCAAGCGCGGCTGCTCG 302
Qy 118 ProleuMetArgGlnTyrGlyPheAlaTyrProGluAargMetSerCysAspArgLeuPro 137
Db 303 CCGCTGAGCGCGAGTACGAGCTTCTGCGCGCGCGCAAGAGCTTGAGACCGCTCCG 362
Qy 138 ValLeuGlyArgAspAlaGluValleuCysMetAspTyrAsnaArgserGluAlaThrThr 157
Db 363 GTCTGAGCGCGCGAGCGCGAGGCTCTCTGATGATTAACCAAGCAAGCAACCGCGCTC 422
Qy 158 AlaProProArgProPheProAlaLysProThrleuProGlyProProGlyAlaProAla 177
Db 423 GCGCGCGCGAGCGCTTTCAGCGCAAGCGCCATTCAGGCGCGCGCGCGCGCGCGC 482
Qy 178 SerGlyGlyGluCyProAlaGlyGlyProPheValCysLysCysArgGluProPheVal 197
Db 483 TCGGCGGCGAGATGCCGCTGCGGCGCGCGCTTGTGTGCAAGTGTGCGAGCGCTTGTG 542
Qy 198 ProileuLysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsn 217
Db 543 CCTCTGAAAGAGTCAACCGCTTACACAAAGGTGCGACCGCGCAAGTCCCACTGCGG 602
Qy 218 CysAlaValProCyTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
Db 603 TCGCGGTAACCTCTGTACCAACCGCTTCTGAGTGCAGCGAGCGGAGCTTGCC 656

RESULT 10

US-60-213-169-11
; Sequence 11, Application US/60213169
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000699
; CURRENT APPLICATION NUMBER: US/60/213,169
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 785
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(785)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-169-11

Alignment Scores:

Pred. No.: 2,87e-57 Length: 785
Score: 1048.00 Matches: 185
Percent Similarity: 95.90% Conservatve: 2
Best Local Similarity: 94.87% Mismatches: 8
Query Match: 80.00% Indels: 0
DB: 65 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-213-169-11 (1-785)

Qy 41 CysArgGlyLysGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 11 TCGACAGCTGAGGTTCTACTATGAGAGATCCCAACAGTTCAACAGAGCGAG 70
Qy 61 AspGluAlaGlyLeuGlnValHisGlnPheThrProLeuValGlnIleGlnCysSerPro 80


```
DB 71 GACGAGGCGGCGCTGAGGTGACACGAGGCGTGGCCCTGCTGAGATTCATGCTGCGCG 130
QY 81 AAspleuAArgPhePheLeuCySerThrmTyTrhProIleCySleuProAspTyTrhIleu 100
DB 131 GACCTGGCTTCTTCTTATGCTATGTAACAGCCCATCTGTGTGCCAGTACACACAG 190
QY 101 ProLeuProProCySerServalCysGluArgAlaIleuAglyCysSerProLeuMet 120
DB 191 CCGCTGGCGCCCTGCGCTCGGTGTGCGAGCGGCCCAAGCGCGCTGCTGCGCGTGTG 250
QY 121 ArgGlnTyGlyPheAlaTrpProGluArgMetSerCyAspArgLeuProValLeuGly 140
DB 251 CCGCAGTACGCGCTTCCCTGCGCGCCGAGCCCATGATGCTGCGACCGCTCCCGGTGCTGGGC 310
QY 141 ArgAspAlaGluValLeuCySerMetAspTyTrhAsnArgServalThrAlaProPro 160
DB 311 CCGGACGCGCGAGTCTCTGTGATGATTAACACGAGCGAGGCCACACGCGCGCCCGCC 370
QY 161 ArgProPheProAlaIleuProThrLeuProGlyProProGlyAlaProAlaSerGly 180
DB 371 AGCGCTTTCACGACCAAGCCACCTTCAGCGCCCGCCGAGGCGCGCGCTGCGGGGCG 430
QY 181 GluCySProAlaGlyGlyProPheValCysLysCyAspArgGluProPheValProIleu 200
DB 431 GAATGCCCCGCTGGGGGCGCGCTTCTGTGCAAGTGTGCGAGCCCTTGTGCGCATTTCTG 490
QY 201 LysGluSerHisProLeuTyTrhAsnLysValArgThrGlyGlnValProAsnCySAlaVal 220
DB 491 AAGGAGTCAACACCCGCTCTACACACAGGTGCGAGCGGCGAGGTGCCAATGCGCGGTA 550
QY 221 ProCySTyGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB 551 CCTGTCTACAGCGCTCTTCAGTGCGAGCGAGCGACGCTGCGCC 595
```

```
RESULT 11
US-60-213-170-11
; Sequence 11, Application US/60213170
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00699
; CURRENT APPLICATION NUMBER: US/60/213,170
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 785
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(785)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-170-11
```

```
Alignment Scores:
Pred. No.: 2,87e-57 Length: 785
Score: 1048.00 Matches: 185
Percent Similarity: 95.90% Conservative: 2
Best Local Similarity: 94.87% Mismatches: 8
Query Match: 80.00% Indels: 0
DB: Gaps: 0
```

US-09-847-102a-68 (1-235) x US-60-213-170-11 (1-785)

```
QY 41 CysArgGlyIleGlyTyTrhAsnLeuThrHisMetProAsnGlnPheAsnHisAspTrhGln 60
DB 11 TGCAGACCTGCGAGGTCTACTCTAGAGAGATCCCGACACAGTTCACACACGACGAG 70
QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80
```

```
DB 71 GACGAGGCGGCGCTGAGGTGACACGAGGCGTGGCCCTGCTGAGATTCATGCTGCGCG 130
QY 81 AAspleuAArgPhePheLeuCySerThrmTyTrhProIleCySleuProAspTyTrhIleu 100
DB 131 GACCTGGCTTCTTCTTATGCTATGTAACAGCCCATCTGTGTGCCAGTACACACAG 190
QY 101 ProLeuProProCySerServalCysGluArgAlaIleuAglyCysSerProLeuMet 120
DB 191 CCGCTGGCGCCCTGCGCTCGGTGTGCGAGCGGCCCAAGCGCGCTGCTGCGCGTGTG 250
QY 121 ArgGlnTyGlyPheAlaTrpProGluArgMetSerCyAspArgLeuProValLeuGly 140
DB 251 CCGCAGTACGCGCTTCCCTGCGCGCCGAGCCCATGATGCTGCGACCGCTCCCGGTGCTGGGC 310
QY 141 ArgAspAlaGluValLeuCySerMetAspTyTrhAsnArgServalThrAlaProPro 160
DB 311 CCGGACGCGCGAGTCTCTGTGATGATTAACACGAGCGAGGCCACACGCGCGCCCGCC 370
QY 161 ArgProPheProAlaIleuProThrLeuProGlyProProGlyAlaProAlaSerGly 180
DB 371 AGCGCTTTCACGACCAAGCCACCTTCAGCGCCCGCCGAGGCGCGCGCTGCGGGGCG 430
QY 181 GluCySProAlaGlyGlyProPheValCysLysCyAspArgGluProPheValProIleu 200
DB 431 GAATGCCCCGCTGGGGGCGCGCTTCTGTGCAAGTGTGCGAGCCCTTGTGCGCATTTCTG 490
QY 201 LysGluSerHisProLeuTyTrhAsnLysValArgThrGlyGlnValProAsnCySAlaVal 220
DB 491 AAGGAGTCAACACCCGCTCTACACACAGGTGCGAGCGGCGAGGTGCCAATGCGCGGTA 550
QY 221 ProCySTyGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB 551 CCTGTCTACAGCGCTCTTCAGTGCGAGCGAGCGACGCTGCGCC 595
```

```
RESULT 12
US-60-213-169-463
; Sequence 463, Application US/60213169
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00699
; CURRENT APPLICATION NUMBER: US/60/213,169
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 696
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(696)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-169-463
```

```
Alignment Scores:
Pred. No.: 3,66e-55 Length: 696
Score: 1014.00 Matches: 178
Percent Similarity: 99.45% Conservative: 2
Best Local Similarity: 98.34% Mismatches: 1
Query Match: 77.40% Indels: 0
DB: Gaps: 0
```

US-09-847-102a-68 (1-235) x US-60-213-169-463 (1-696)

```
QY 55 PheAsnHisAspTrhGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuVal 74
DB 2 TTCAACACAGACACACGAGGAGCGGCGCTGAGAGGTGACACAGAGGCGCGCTGTG 61
QY 75 GluIleGlnCysSerProAspLeuArgPhePheLeuCySerThrmTyTrhProIleCys 94
```



```

Db      490 AAGGCGGCTGCTCGCGCTGATGCGCCAGTACGGCTCGCGCCGCGCATGAGC 431
QY      133 CYSASPTGLENPROVALLEUGLYARGAPALAGLVALLEUCYSMETASPTYRANARG 152
Db      430 TGGACCGGCTCCCGGTGTGGGCGCGACGCCGAGCTCTGTGACATGATTAACAACCC 371
QY      153 SERGLUALATHRTHRILABPROAARGPROPHETPROALALYSPROTHREUPROGLIYPRO 172
Db      370 AAGGAGGCCACACGCGCGCCGCCAGGCTTCCAGGCCACAGCCCTTCCAGGCCCG 311
QY      173 PROGLIYALPROALASERGLYGLIUCYSPROALAGLYLPROPHETVALCYSLYSCYS 192
Db      310 CCAGGCGCGCCCGCGCTCGGCGGCGAATGCGCCGCTGCGGCGCCGCTTCTGTGCAAGTGT 251
QY      193 ARGGLUPROPHETVALPROILLEULYSGIUSERHISPROLEUTYRASNLYSVALARGTHR 212
Db      250 CCGGAGCCCTTCTGTGCTCAATCTGAAGAGTCAACCCGCTTCAACAAGGTGCGGAGC 191
QY      213 GLYGLIYVALPROASNLYSVALAVALPROCYSTYRGLINPROSERPHESERIALAASPGIYARG 232
Db      190 GCGCAGGTGCCCACTGCGCGCGGTACCCCTGTACACCCGCTTCACTGAGTCCGACGAGCC 131
QY      233 THRPHETALA 235
Db      130 ACGTTGCCC 122

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RESULT 15

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US-60-178-308-1287/c
/ Sequence 1287, Application US/60178308
/ GENERAL INFORMATION:
/ APPLICANT: Bonazzi, Vivien
/ TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
/ TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
/ TITLE OF INVENTION: PROTEINS, AND USES THEREOF
/ FILE REFERENCE: CL000204
/ CURRENT APPLICATION NUMBER: US/60178,308
/ CURRENT FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 344
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1287
/ LENGTH: 611
/ TYPE: DNA
/ ORGANISM: HUMAN
US-60-178-308-1287

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Alignment Scores:

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Pred. No.: 2,98e-49 Length: 611
Score: 920.00 Matches: 162
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.39% Mismatches: 0
Query Match: 70.23% Indels: 0
DB: 61 Gaps: 0

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US-09-847-102a-68 (1-235) x US-60-178-308-1287 (1-611)

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QY      73 LEUVALGLIUIELGLNYSSEPTROASPLEUARGPHEPHEUCYSMTMETYRTHRPRO 92
Db      610 CTGGTGAAGATCCAAATGCTGCGCGACCTGCGCTTCTCTATGCTATGATACACCCC 551
QY      93 IIECYSLUENPROASPTYRHSISYSPROLEUPROCYASISSEVALCYSGIUALGALA 112
Db      550 ATCTGTCTGCGCGCATACCAACAGCGCTGCGCGCTGCGCGCTGCGGTGTGCGAGCGCGCC 491
QY      113 LYSALAGLYCYSESEPTOLEUWETARGINTYRGLYPHEALATRPROGLIYARGMETSER 132
Db      490 AAGGCGGCTGCTCGCGCTGARGCGCCAGTACGCTTCCGCTGCGCGCCGAGCGCATGAGC 431
QY      133 CYSASPTGLENPROVALLEUGLYARGAPALAGLVALLEUCYSMETASPTYRANARG 152
Db      430 TGGACCGGCTCCCGGTGTGGGCGCGACGCCGAGCTCTGTGACATGATTAACAACCC 371
QY      153 SERGLUALATHRTHRILABPROAARGPROPHETPROALALYSPROTHREUPROGLIYPRO 172

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```

Db      370 AAGGAGGCCACACGCGCGCCGCCAGGCTTCCAGGCCAAGCCACCCCTTCCAGGCCCG 311
QY      173 PROGLIYALPROALASERGLYGLIUCYSPROALAGLYLPROPHETVALCYSLYSCYS 192
Db      310 CCAGGCGCGCCCGCGCTCGGCGGCGAATGCGCCGCTGCGGCGCCGCTTCTGTGCAAGTGT 251
QY      193 ARGGLUPROPHETVALPROILLEULYSGIUSERHISPROLEUTYRASNLYSVALARGTHR 212
Db      250 CCGGAGCCCTTCTGTGCTCAATCTGAAGAGTCAACCCGCTTCAACAAGGTGCGGAGC 191
QY      213 GLYGLIYVALPROASNLYSVALAVALPROCYSTYRGLINPROSERPHESERIALAASPGIYARG 232
Db      190 GCGCAGGTGCCCACTGCGCGCGGTACCCCTGTACACCCGCTTCACTGAGTCCGACGAGCC 131
QY      233 THRPHETALA 235
Db      130 ACGTTGCCC 122

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Search completed: May 23, 2003, 04:40:15
Job time : 2430 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model.

Run on: May 22, 2003, 18:01:48 ; Search time 603 Seconds
(without alignments)
2021.442 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPPSAPSLILLILLAQL.....PNCAPCYOPSEFADERTFA 235

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6438716 seqs, 2593467500 residues
Total number of hits satisfying chosen parameters: 12877432

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_New.*

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6: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
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8: /cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq.*
9: /cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq.*
10: /cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq.*
11: /cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	2334	8	US-10-285-976-48
2	1306	99.7	2674	8	US-10-170-235-22610
3	1250	95.4	1758	9	US-10-144-771-18143
4	824	62.9	2085	9	US-10-311-623-18
5	824	62.9	3182	8	US-10-170-235-35769
6	824	62.9	3182	11	US-60-453-135-1905
7	824	62.9	3195	8	US-10-285-976-54

8	824	62.9	3206	8	US-10-115-678-6	Sequence 6, Appl1
9	824	62.9	3206	8 <td>US-10-112-944-6</td> <td>Sequence 6, Appl1</td>	US-10-112-944-6	Sequence 6, Appl1
10	823.5	62.9	2058	9 <td>US-10-144-771-10276</td> <td>Sequence 10276, A</td>	US-10-144-771-10276	Sequence 10276, A
11	479.5	36.6	2043	9 <td>US-10-144-771-12343</td> <td>Sequence 12343, A</td>	US-10-144-771-12343	Sequence 12343, A
12	477	36.4	1983	8 <td>US-10-285-976-42</td> <td>Sequence 42, Appl1</td>	US-10-285-976-42	Sequence 42, Appl1
13	477	36.4	1983	9 <td>US-10-225-567A-581</td> <td>Sequence 381, Appl</td>	US-10-225-567A-581	Sequence 381, Appl
14	472.5	36.1	1933	8 <td>US-10-170-235-33965</td> <td>Sequence 33965, A</td>	US-10-170-235-33965	Sequence 33965, A
15	472.5	36.1	1933	11 <td>US-60-453-135-1905</td> <td>Sequence 1905, Ap</td>	US-60-453-135-1905	Sequence 1905, Ap
16	472.5	36.1	1933	11 <td>US-60-453-135-1905</td> <td>Sequence 1905, Ap</td>	US-60-453-135-1905	Sequence 1905, Ap
17	472.5	36.1	211587	5 <td>US-09-948-128-281</td> <td>Sequence 281, Ap</td>	US-09-948-128-281	Sequence 281, Ap
18	461	35.2	3851	1 <td>PCT-US02-24567-26</td> <td>Sequence 26, Appl1</td>	PCT-US02-24567-26	Sequence 26, Appl1
19	461	35.2	3851	8 <td>US-10-285-976-52</td> <td>Sequence 52, Appl1</td>	US-10-285-976-52	Sequence 52, Appl1
20	461	35.2	3851	8 <td>US-10-210-120-26</td> <td>Sequence 26, Appl1</td>	US-10-210-120-26	Sequence 26, Appl1
21	440.5	33.6	2262	9 <td>US-10-144-771-16597</td> <td>Sequence 16597, A</td>	US-10-144-771-16597	Sequence 16597, A
22	417	31.8	1929	9 <td>US-10-144-771-691</td> <td>Sequence 691, Appl</td>	US-10-144-771-691	Sequence 691, Appl
23	415	31.7	4350	8 <td>US-10-285-976-40</td> <td>Sequence 40, Appl1</td>	US-10-285-976-40	Sequence 40, Appl1
24	415	31.7	4537	8 <td>US-10-170-235-19892</td> <td>Sequence 19892, A</td>	US-10-170-235-19892	Sequence 19892, A
25	406	31.0	4837	8 <td>US-10-062-674-1978</td> <td>Sequence 1978, Ap</td>	US-10-062-674-1978	Sequence 1978, Ap
26	399	30.5	2184	8 <td>US-10-285-976-56</td> <td>Sequence 56, Appl1</td>	US-10-285-976-56	Sequence 56, Appl1
27	399	30.5	2184	9 <td>US-10-342-887-920</td> <td>Sequence 920, Appl</td>	US-10-342-887-920	Sequence 920, Appl
28	399	30.5	2405	8 <td>US-10-170-235-19899</td> <td>Sequence 19899, A</td>	US-10-170-235-19899	Sequence 19899, A
29	398	30.4	4540	1 <td>PCT-US03-03194-3422</td> <td>Sequence 3422, Ap</td>	PCT-US03-03194-3422	Sequence 3422, Ap
30	398	30.4	4540	11 <td>US-60-436-643-3422</td> <td>Sequence 3422, Ap</td>	US-60-436-643-3422	Sequence 3422, Ap
31	394.5	30.1	1779	9 <td>US-10-144-771-46172</td> <td>Sequence 46172, A</td>	US-10-144-771-46172	Sequence 46172, A
32	388	29.6	2270	9 <td>US-10-017-161-799</td> <td>Sequence 799, Appl</td>	US-10-017-161-799	Sequence 799, Appl
33	387	29.5	658	8 <td>US-10-405-027-61</td> <td>Sequence 61, Appl</td>	US-10-405-027-61	Sequence 61, Appl
34	387	29.5	1746	1 <td>PCT-US02-41414-1522</td> <td>Sequence 1522, Ap</td>	PCT-US02-41414-1522	Sequence 1522, Ap
35	387	29.5	2811	1 <td>PCT-US02-41414-1521</td> <td>Sequence 1521, Ap</td>	PCT-US02-41414-1521	Sequence 1521, Ap
36	387	29.5	3254	8 <td>US-10-170-235-22704</td> <td>Sequence 22704, A</td>	US-10-170-235-22704	Sequence 22704, A
37	387	29.5	3260	8 <td>US-10-285-976-58</td> <td>Sequence 58, Appl1</td>	US-10-285-976-58	Sequence 58, Appl1
38	387	29.5	22804	1 <td>PCT-US02-41414-1520</td> <td>Sequence 1520, Ap</td>	PCT-US02-41414-1520	Sequence 1520, Ap
39	380.5	29.0	1909	1 <td>PCT-US02-41225A-203</td> <td>Sequence 203, Appl</td>	PCT-US02-41225A-203	Sequence 203, Appl
40	380.5	29.0	1909	5 <td>US-09-873-367C-282</td> <td>Sequence 282, Appl</td>	US-09-873-367C-282	Sequence 282, Appl
41	380	28.0	978	1 <td>PCT-US02-41225A-204</td> <td>Sequence 204, Appl</td>	PCT-US02-41225A-204	Sequence 204, Appl
42	372.5	28.4	1738	7 <td>US-09-948-016-1873</td> <td>Sequence 1873, Ap</td>	US-09-948-016-1873	Sequence 1873, Ap
43	372.5	28.4	2151	8 <td>US-10-170-235-6760</td> <td>Sequence 6760, Ap</td>	US-10-170-235-6760	Sequence 6760, Ap
44	372.5	28.4	2151	11 <td>US-60-453-135-4168</td> <td>Sequence 4168, Ap</td>	US-60-453-135-4168	Sequence 4168, Ap
45	372.5	28.4	2151	11 <td>US-60-453-050-4168</td> <td>Sequence 4168, Ap</td>	US-60-453-050-4168	Sequence 4168, Ap

ALIGNMENTS

RESULT 1
US-10-285-976-48
Sequence 48, Application US/10285976
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leon, Lorenzo M.
APPLICANT: Carr, Maripat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 2334
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzleds (Fzds)
US-10-285-976-48
Alignment Scores:

Pred. No.: 3,17e-80 Length: 2334
 Score: 1310.00 Matches: 235
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-847-102a-68 (1-235) x US-10-285-976-48 (1-2334)

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QY      1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeu 20
DB      321 ATGGCTCGGCTGACCCATCCGCGCCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 380
QY      21 ValGlyArgAlaAlaAlaAlaSerIysAlaProValCysGlnGlnIleThrValPromet 40
DB      381 GTGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 440
QY      41 CysArgGlyIleGlyTyrAsnLeuThrIsmetProAsnGlnPheAsnHisAspThrGln 60
DB      441 TGCCTGGCGATCGGCTACCACTGACGACATGCCCCAACCAGTTCACACACGACGACG 500
QY      61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlnIleGlnCysSerPro 80
DB      501 GACGAGCGGCGCTGAGGTGACCACTTCCTGCGCTGCGTGGAGATCCAAATGCTGCGCG 560
QY      81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisIys 100
DB      561 GACCTCGCTTCTTCTTATGACATATGATACAGCCCATCTGTCGCCGACATACCAAG 620
QY      101 ProLeuProProCysArgSerValCysGluArgAlaIysAlaGlyCysSerProLeuMet 120
DB      621 CCGCTGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
QY      121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
DB      681 CGGCACTACGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740
QY      141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGlnIleThrAlaProPro 160
DB      741 CGGAGCGCGAGGCTCTCTGCAATGATTCACACGACGAGGACCAACGCGCGCGCC 800
QY      161 ArgProPheProAlaIysProThrLeuProGlyProProGlyAlaProAlaSerGlyIy 180
DB      801 AGGCTTTTCCCAAGCCCAAGCCCACTTCACAGGCCCGCGCGCGCGCGCGCGCGCG 860
QY      181 GluCysProAlaGlyGlyProPheValCysIysCysArgGluProPheValProIleLeu 200
DB      861 GAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 920
QY      201 LysGlnSerHisProLeuTyrAsnIysValArgThrGlyGlnValProAsnCysAlaVal 220
DB      921 AAGGAGTACACACCGCTCTACCAACAGGTGCGGACCGGCGCGCGCGCGCGCGCG 980
QY      221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB      981 CCTGCTACCAAGCGCTCTTCAATGTCGACGAGCGACGCTTCGCC 1025

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RESULT 2

US-10-170-235-22610

; Sequence 22610, Application US/10170235

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN

; FILE REFERENCE: CL001380

; CURRENT APPLICATION NUMBER: US/10/170,235

; CURRENT FILING DATE: 2003-03-17

; NUMBER OF SEQ ID NOS: 42514

; SEQ ID NO 22610

; LENGTH: 2674

; TYPE: DNA

; ORGANISM: HUMAN

US-10-170-235-22610

Alignment Scores:
 Pred. No.: 6.94e-80 Length: 2674
 Score: 1306.00 Matches: 234
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.57% Mismatches: 0
 Query Match: 99.69% Indels: 0
 DB: 8 Gaps: 0

US-09-847-102a-68 (1-235) x US-10-170-235-22610 (1-2674)

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QY      1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeu 20
DB      482 ATGGCTCGGCTGACCCATCCGCGCCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
QY      21 ValGlyArgAlaAlaAlaAlaSerIysAlaProValCysGlnGlnIleThrValPromet 40
DB      542 GTGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 601
QY      41 CysArgGlyIleGlyTyrAsnLeuThrIsmetProAsnGlnPheAsnHisAspThrGln 60
DB      602 TGCCTGGCGATCGGCTACCACTGACGACATGCCCCAACCAGTTCACACACGACGACG 661
QY      61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlnIleGlnCysSerPro 80
DB      662 GACGAGCGGCGGCTGAGGTGACCACTTCCTGCGCTGCGTGGAGATCCAAATGCTGCG 721
QY      81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisIys 100
DB      722 GACCTCGCTTCTTCTTATGACATATGATACAGCCCATCTGTCGCCGACATACCAAG 781
QY      101 ProLeuProProCysArgSerValCysGluArgAlaIysAlaGlyCysSerProLeuMet 120
DB      782 CCGCTGCGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 841
QY      121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
DB      842 CGGCACTACGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
QY      141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGlnIleThrAlaProPro 160
DB      902 CGGAGCGCGAGGCTCTCTGCAATGATTCACACGACGAGGACCAACGCGCGCGCC 961
QY      161 ArgProPheProAlaIysProThrLeuProGlyProProGlyAlaProAlaSerGlyIy 180
DB      962 AGGCTTTTCCCAAGCCCAAGCCCACTTCACAGGCCCGCGCGCGCGCGCGCGCG 1021
QY      181 GluCysProAlaGlyGlyProPheValCysIysCysArgGluProPheValProIleLeu 200
DB      1022 GAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1081
QY      201 LysGlnSerHisProLeuTyrAsnIysValArgThrGlyGlnValProAsnCysAlaVal 220
DB      1082 AAGGAGTACACCCCGCTCTACCAACAGGTGCGGACCGGCGCGCGCGCGCGCGCG 1141
QY      221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB      1142 CCTGCTACCAAGCGCTCTTCAATGTCGACGAGCGACGCTTCGCC 1186

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RESULT 3

US-10-144-771-18143

; Sequence 18143, Application US/10144771

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF

; FILE REFERENCE: CL001321

; CURRENT APPLICATION NUMBER: US/10/144,771

; CURRENT FILING DATE: 2002-05-15

; NUMBER OF SEQ ID NOS: 47235

; SEQ ID NO 18143

; LENGTH: 1758

; TYPE: DNA

; ORGANISM: HUMAN

US-10-144-771-18143

Alignment Scores:

Pred. No.: 2,94e-76 Length: 1758
 Score: 1250.00 Matches: 224
 Percent Similarity: 97.02% Conservative: 4
 Best Local Similarity: 95.32% Mismatches: 7
 Query Match: 95.42% Indels: 0
 DB: 9 Gaps: 0

US-09-847-102a-68 (1-235) x US-10-144-771-18143 (1-1785)

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QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
DB 1 ATGGCTCGACCCGACCCGCTCGCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTG 60
QY 21 ValGlyArgAlaAlaAlaSerLeuAlaProValCysGlnGlnLeuThrAlaProMet 40
DB 61 GTGGGCGGGGACGGCGCGCTCCAGAGCGCGGCTGTGCGAGAAATCAGGATGCCCATG 120
QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
DB 121 TCCCGAGGATGGGCTGACAACTGACGACGACATGCCAACCACTTCAACCATACAGCGAG 180
QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlnIleGlnCysSerPro 80
DB 181 GACGAAGCAGCGCTGGAGGTGCACCAATCTGGCGCTTGAGATCCACTGCTCACCG 240
QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
DB 241 GACCTGCGCTTCTCTCTGCTCTGCTTAAGTACAGCGCCCATCTGTTGCTGACTACCAAG 300
QY 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
DB 301 CCGCTACCACTGCGCTGCTTCCCTGCTGCGAGCGCGGCGGAGCGCGCTGCTGCGCTCAG 360
QY 121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
DB 361 CCGCAGTACGCGCTGCGCTGCGCTGCGCGAGCGCATGAGTGCAGCGCTGCTGCTGCGG 420
QY 141 ArgAspAlaGlnValLeuCysMetAspTyrAsnArgSerGlnAlaThrThrAlaProPro 160
DB 421 GCGGAGCGCGAGGCTTCTGTGATGATTAACCGAAGGAGCAACCGCGCTGCTGCTGCT 480
QY 161 ArgProPheProAlaLysAspProThrLeuProGlyProProGlyAlaProAlaSerGly 180
DB 481 AAGTCTTCCCGGCAACTACCTCCAGAGACCAACGAGGCGCGCTGCTGCTGCGGAGC 540
QY 181 GlnCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeu 200
DB 541 GAGTGCCTCCGAGAGCGCATCCGTGTGCACGTGCGGAGCGCTGCTGCTGCTGCTGCTG 600
QY 201 LysGlnSerHisProLeuTyrHisLysValArgThrGlyGlnValProAsnCysAlaVal 220
DB 601 AAGGAGTCAACACCACTTCAACAAGGTCGACCGGCGCAAGTGCCTCACTGCGGCTG 660
QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB 661 CCTGCTACCACTGCTTCTTCAAGCCGCGAGCGAGCGCACTGCGC 705

```

RESULT 4

US-10-311-623-18

Sequence 18, Application US/10311623

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
 APPLICANT: KALICK, Deborah A.; TRIBOUNEV, Catherine M.
 APPLICANT: YUE, Henry; NGUYEN, Daniel B.
 APPLICANT: TANG, Y. Tom; LAU, Preeti G.
 APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
 APPLICANT: LU, Dyrung Aina M.; GRAUL, Richard C.
 APPLICANT: YAO, Monique G.; BURFORD, Neil
 APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
 APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.

```

; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1534444CB1
US-10-311-623-18

```

Alignment Scores:

Pred. No.: 5.24e-47 Length: 2085
 Score: 824.00 Matches: 161
 Percent Similarity: 67.66% Conservative: 21
 Best Local Similarity: 59.85% Mismatches: 39
 Query Match: 62.90% Indels: 48
 DB: 9 Gaps: 8

US-09-847-102a-68 (1-235) x US-10-311-623-18 (1-2085)

```

QY 11 SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaSer 28
DB 31 TCGCTGCTGCGCGCTTGGCGCTGCTGCGAGCGCTTACCGGCGCGCGCGCGCTGCGG 90
QY 29 LysAlaProValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeu 48
DB 91 AAGGAGCTGAGCATGCAAGATGATCACCGTGCCTGTGTAAGGCGCATCGCTACCACTAC 150
QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
DB 151 ACCTACATGCCCAACAGCTTCAACCAACGACGAGCGAGCGCGCTGAGGTGAC 210
QY 69 GlnPheTrpProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
DB 211 CAGTTCTGCGCGCTGCTGAGATTCAGTCTGCGCGCATCTCAACTTCTTCTGTCAGC 270
QY 89 MetTyrThrProIleCysLeuProAspTyrHisLysProLeuProProCysArgSerVal 108
DB 271 ATGTACAGCGCCATCTGCTAGAGACTACAAAGGCGCGCTGCGCGCTGCGGCTG 330
QY 109 CysGluAlaGlyAlaGlyCysSerProLeuMetLysGlnTyrGlyPheAlaTrpPro 128
DB 331 TCCGAGCGCGCAAGCGCGGCTGCGCGCTGCTCACTGCGCGAGTACGCTTGCCTGCGC 390
QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMet 148
DB 391 GACCGCATGCGCTGCGAGCGGCTGCGCGAGCAAGCG---AACCTGACACGCTGTGCTG 447
QY 149 AspTyrAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
DB 448 GACTCAACACCGACGACCTTACCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 507
QY 166 LysProThrLeuProGly-----ProProGly 174
DB 508 CCGCGG-----CCCGGAGACAGCGCGCTTGGGCGAGCGGCGCACGCGCGCGCGCGG 561

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Db      211 CAGTTTCGCGCGCTGATGAGATCCAGTCTGCGCCGAGTCTAAGTTCTTCTGTCAGC 270
Qy      89 MetTyrrhProIleCyseuProAspTyrrhIshyProleuProProCyAspArgSerVal 108
Db      271 ATGTACAGCCCATCTGCTTAGAGACTTACAGAGACCGCTGCGCGCTGCGCGCTGCGG 330
Qy      109 CyseGuAArgAlaValAlaGlyCyseSerProleuMetArgGlnTyrrGlyPheAlaTrpPro 128
Db      331 TCCGAGCGCGCCAGAGCGCGCTGCGCGCGCTCATGCTGCGCAGTACGCGCTTCCGCGCC 390
Qy      129 GUAArgMetSerCyAspArgLeuProValLeuGluArgAspAlaGluValLeuCyseMet 148
Db      391 GACCGCATGCGCTGCGAGCGCGCTGCGCGCGAGCAAGGC---AACCTGACACGCTGTGCAATG 447
Qy      149 AspTyrrhAsnArgSerGluAlaThrAla-----ProProArgProPheProAla 165
Db      448 GACTCAACACCGACCGACTTAACACCGCGCGCCAGCGCGCGCGCGCGCGCTGCGCGCG 507
Qy      166 LysProThrLeuProGly-----ProProGly 174
Db      508 CCGCGG-----CCGCGCGAGCAGCGCGCTTCCGCGAGCGCGCCAGCGCGCGCGCGG 561
Qy      175 Ala----- 175
Db      562 GCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 621
Qy      176 ProAlaSerGlyGly-----GluCyAspProAlaGlyGlyProPheVal 189
Db      622 CCAAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 681
Qy      190 -----CyalyCyAspArgGluProPheValProIleuLysGluSerHisPro 205
Db      682 TCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTATGCTAGCGCTCCAGCGAGCGCGCCAC 741
Qy      206 LeuTyrrhAsnLysValArgThrGlyGlnValProAsnCyAspAlaValProCySerTyrrGlnPro 225
Db      742 CTCTCAACCGCGGTCAAGACAGCGCGCATGCTACTGCGCGCTGCTGCGCCACCAACCC 801
Qy      226 SerPheSerAlaAspGluArgThrPhe 234
Db      802 TTTTTCAGCCAGAGCAGCGCGCGCTTC 828

RESULT 7
US-10-285-976-54
; Sequence 54, Application US/10285976
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leonh, Lorenzo M.
; APPLICANT: Corr, Maridat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; FILE REFERENCE: 023070-130320US
; CURRENT APPLICATION NUMBER: US/10/285,976
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human frizzled8 (Fzd8)
US-10-285-976-54
Alignment Scores:

```

```

Pred. No.: 8.5e-47 Length: 3195
Score: 824.00 Matches: 161
Percent Similarity: 67.66% Conservative: 21
Best Local Similarity: 59.85% Mismatches: 39
Query Match: 52.90% Indels: 48
DB: 8 Gaps: 8

US-09-847-102a-68 (1-235) x US-10-285-976-54 (1-3195)
Qy      11 SerLeuLeu-----LeuLeuLeuValAlaGluValAlaAlaAlaSer 28
Db      36 TCGCTGCTGCGCGCGCTTGGCGCTGCTGCAAGCGCTTACGGCGCGCGCGCGCGCGCG 95
Qy      29 LysAlaProValCyseGlnGluIleThrValProMetCyAspArgIleGlyTyrrhAsnLeu 48
Db      96 AAGAGCTGCGCATGCGCAAGAGATCACTGCGCGCTGTGTAAAGGCGATCGCTACCAATAC 155
Qy      49 ThrhIshMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
Db      156 ACCTACATGCGCCAAATCAAGTTCAACCAACAGACAGCAAGAGCGCGCGCTGAGAGTGAC 215
Qy      69 GlnPheTrpProLeuValGluIleGlnCyseSerProAspLeuArgPheLeuCySerThr 88
Db      216 CAGTTCTGCGCGCGCTGCTGAGATCCAGTCTGCGCGCGCTTCAAGTTCTTCTGTCAGC 275
Qy      89 MetTyrrhProIleCyseuProAspTyrrhIshyProleuProProCyAspArgSerVal 108
Db      276 ATGTACAGCCCATCTGCTTAGAGACTTACAGAGACCGCGCTGCGCGCGCTGCGCGT 335
Qy      109 CyseGuAArgAlaValAlaGlyCyseSerProleuMetArgGlnTyrrGlyPheAlaTrpPro 128
Db      336 TCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATGCGCGCGCTTCCGCGCGCG 395
Qy      129 GUAArgMetSerCyAspArgLeuProValLeuGluArgAspAlaGluValLeuCyseMet 148
Db      336 GACCGCATGCGCTGCGAGCGCGCTGCGCGCGAGCAGCAGC---AACCTGACACGCTGTGCAATG 452
Qy      149 AspTyrrhAsnArgSerGluAlaThrAla-----ProProArgProPheProAla 165
Db      453 GACTCAACACCGACCGACTTAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 512
Qy      166 LysProThrLeuProGly-----ProProGly 174
Db      513 CCGCGG-----CCGCGCGAGCAGCGCGCTTCCGCGAGCGCGCGCGCGCGCGCGCG 566
Qy      175 Ala----- 175
Db      567 GCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 626
Qy      176 ProAlaSerGlyGly-----GluCyAspProAlaGlyGlyProPheVal 189
Db      627 CCAAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 686
Qy      190 -----CyalyCyAspArgGluProPheValProIleuLysGluSerHisPro 205
Db      687 TCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTATGCTAGCGCTTCCAGCGAGCGCGCAC 746
Qy      206 LeuTyrrhAsnLysValArgThrGlyGlnValProAsnCyAspAlaValProCySerTyrrGlnPro 225
Db      747 CTCTCAACCGCGGTCAAGACAGCGCGCATGCTACTGCGCGCTGCTGCGCCACCAACCC 806
Qy      226 SerPheSerAlaAspGluArgThrPhe 234
Db      807 TTTTTCAGCCAGAGCAGCGCGCGCTTC 833

RESULT 8
US-10-115-678-6
; Sequence 6, Application US/10115678
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezh
; APPLICANT: Zhang, Jie

```


PRIOR FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 924
 SOFTWARE: pf_fl_genes Version 5.0
 SEQ ID NO 6
 LENGTH: 3206
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (381)..(2462)
 US-10-112-944-6

Alignment Scores:
 Pred. No.: 8.53e-47 Length: 3206
 Score: 824.00 Matches: 161
 Percent Similarity: 67.66% Conservative: 21
 Best Local Similarity: 59.85% Mismatches: 39
 Query Match: 62.90% Indels: 48
 DB: Gaps: 8

US-09-847-102a-68 (1-235) x US-10-112-944-6 (1-3206)

QY 11 SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaSer 28
 DB 411 TCGCTGCTGCGCCGCTGCGCTGCTGCGAGCCCTCTAGCGCGCTGCGCCGCTCGGCC 470
 QY 29 LysAlaProValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyraSerLeu 48
 DB 471 AAGAGCTGGCATGCCAAGATCAACCGCTGCTGTGAAGGATCGGCTCAACAATC 530
 QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGlnValHis 68
 DB 531 ACCTCATGCTCCCAATCAGTTCAACCAACGACGACGCAAGAGCGCGCTGAGGTGCAC 590
 QY 69 GlnPheTrpProLeuValGlnIleGlnCysSerProAspLeuArgPheLeuCysThr 88
 DB 551 CAGTTTGGCGCTGCTGAGATCCAGTGTCTGCGCCGATCTCAAGTTCTTCTGTGCAC 650
 QY 89 MetTyrrProIleCysLeuProAspTyrrHisLysProLeuProProCysArgSerVal 108
 DB 651 ATGTACAGCCCATCTGCTAGAGACTACAAAGACCGCTGCGCCCTCGCTCGGTG 710
 QY 109 CysGlnArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrrGlyPheAlaTrpPro 128
 DB 711 TCGAGCGCGCCAGAGCGCGCTGCGCGCTCATGCGCCAGTACGCGCTTGCCTGCGCC 770
 QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMet 148
 DB 771 GACCCCATGCTGCTGCGAGCCGCTGCCGAGCAAGGC--AACCTGACACGCTGTGCATG 827
 QY 149 AspTyrrAsnArgSerGlnAlaThrThrAla-----ProProArgProPheProAla 165
 DB 828 GACTACAAACGCGACGCACTTAACACCGCGCGCCAGCCCGCGCGCTTGCCTGCGCC 887
 QY 166 LysProThrLeuProGly-----ProProGly 174
 DB 888 CCGCGC-----CCGCGAGACGCGCCTTCCGCGAGCGCGCACGCGCGCGCGGG 941
 QY 175 Ala----- 175
 DB 942 GCCAGAGCCCGCACCGCGCGCGCGAGGCGGTGCGCGCGGAGCGCGCGCGCGCC 1001
 QY 176 ProAlaSerGlyIle-----GluCysProAlaGlyIleGlyProPheVal 189
 DB 1002 CCAAGCTCGCGCGCGCGCGGTGCGGAGAGCGCGCGCCCTTGCCTGCGCGCGCTCC 1061
 QY 190 -----CysLysCysArgGlnProPheValProIleLeuLysGlnSerHisPro 205
 DB 1062 TCCGAGCCCGGTGCGAGTGCAGCGCGCTATGTAGTGAAGGTGTCCAGAGCGCACCG 1121
 QY 206 LeuTyrrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyrrGlnPro 225
 DB 1122 CTCTACACCGGCTCAAGACAGCGCATGCTTAAGTGTGCGCTGCTGCGCACAAACCC 1181

QY 226 SerPheSerAlaAspGluArgThrPhe 234
 DB 1182 TTTTTCACGACGAGACGCGGCTTC 1208

RESULT 10

US-10-144-771-10276
 Sequence 10276, Application US/10144771
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig
 TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 FILE REFERENCE: CLO01321
 CURRENT APPLICATION NUMBER: US/10/144,771
 CURRENT FILING DATE: 2002-05-15
 NUMBER OF SEQ ID NOS: 47235
 SEQ ID NO 10276
 LENGTH: 2058
 TYPE: DNA
 ORGANISM: HUMAN
 US-10-144-771-10276

Alignment Scores:
 Pred. No.: 5.58e-47 Length: 2058
 Score: 823.50 Matches: 159
 Percent Similarity: 69.06% Conservative: 24
 Best Local Similarity: 60.00% Mismatches: 39
 Query Match: 62.86% Indels: 43
 DB: Gaps: 8

US-09-847-102a-68 (1-235) x US-10-144-771-10276 (1-2058)

QY 11 SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaSer 28
 DB 31 TCGCTCTAGCGCCGCTTGGCGCTGCTTACAGGCTCTACAGCGCGCTGCGCGCTTGC 90
 QY 29 LysAlaProValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyraSerLeu 48
 DB 91 AAGAGCTGGCGTCCCAAGATCAACGCTGCTGTCAAGGATCGGCTTACCAATC 150
 QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGlnValHis 68
 DB 151 ACTTACATGCGCCCAACCATTTCAACCAACGACGACGCAAGTGAAGCGCGCTAGAGTGCAC 210
 QY 69 GlnPheTrpProLeuValGlnIleGlnCysSerProAspLeuArgPheLeuCysThr 88
 DB 211 CAGTTTGGCGCTGCTGAGATACAGTGTCTCCCGGACCTCAAGTTCTTCTGTGTAC 270
 QY 89 MetTyrrProIleCysLeuProAspTyrrHisLysProLeuProProCysArgSerVal 108
 DB 271 ATGTACAGCCCATCTGCTGAGAGACTACAAAGACCTTGCCTGTGTGCTGTG 330
 QY 109 CysGlnArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrrGlyPheAlaTrpPro 128
 DB 331 TGTGAACGCGCCCAAGCGCGCTGCGCTCATGCGCCAGTACGCGCTTGTGCGCT 390
 QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMet 148
 DB 391 GACCCCATGCTGCTGAGTGTGCTTGCAGAGCAGGC--AACCGAGACACTGTGTGATG 447
 QY 149 AspTyrrAsnArgSerGlnAlaThrThrAla-----ProProArgProPheProAla 165
 DB 448 GACTACAAACGCGACGCACTCAACACGCGCGCCAGCCACCGCGCGCTGCTCG 507
 QY 166 LysProThrLeuProGly-----ProProGly 174
 DB 508 CCGCTCTCT--CCGCGAGACGCGCCTTGTGAGCGGCGCACAGCGCGCGCGCAGGG 564
 QY 175 Ala----- 175
 DB 565 GCCAGAGCCCGACATCGTGGCGGACAGTACGAGGCGAGCGGAGACGCGCGCTGCGCC 624
 QY 176 ProAlaSerGlyIleGlyCys-----ProAlaGlyIleGlyProPheVal----- 189


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Db      316  GCCCAGCAAGAACAGAGAGAGCCAGGCTTACAGGTCCAGCTTCTATCCGTGTGAAG 375
Qy      76  IlegiCysSerProAspLeuArgPhePheLeuCySthMetTyThrProIleCySleu 95
      376  GTGAGTGTGTGCGCCGGAAGTGTGCTTTCTCTGTCTCATATGAGCAACCCGTGTGACCC 435
Qy      96  ProAspTyThrAlaLeuProLeuProCySthArgSerValCySgluArgAlaLeuAlaGly 115
      436  GTG---CTGGAACAGAGCCATCCCGCGGTGCTCTATCTGTGAGCGCGCGCCAGAGGC 492
Qy      116  CysSerProLeuMetArgGlnTyArgPheAlaTPrProGluArgMetSerCysAspArg 135
      493  TCGAAGCCCTCATGAACAAGTTCGATTTCAGTGGCCGAGCCGCTGCGTGCAGAC 552
Qy      136  LeuProValLeuGlyArgAspAlaGluValLeuCyMetAspTyArgAsnArgSerGlu--- 154
      553  TTCCCGGCGGACAGGC-----GCCAGCAGATCTGCTGCGGCGAGAACACATCCAGAGAC 606
Qy      155  -----AlaThrThrAlaProProArgProPheProAlaLeuProThrIleu 169
      607  GGAGCTCCCGGCTACTACACACCGCGCGCGCGGAGCTG-----CAGCGGAGTGC 660
Qy      170  ProGlyProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGly----- 186
      661  GGGGCGACCCCGGGTGGCCCGGCGCGCGCGCTCCCGCGCTACGCGCACGCTGAG 720
Qy      187  ---ProPheValCyLeuCyArgGluProPheValProIleLeuLeuGluSerHisPro 205
      721  CACCCCTTCCACTGCGCG-----CGGCTCTCAAGCTG-----CCA 756
Qy      206  LeuTyraAsnLeuValArgThrGlyGlnValProAsnCySAlaValProCySthGlnPro 225
      757  TCCATCTCAGCTACAGATTCTGGGCGAGCGTATGTGTGCGCCCTGC---GAACCT 813
Qy      226  Ser-----PheSerAlaAspGluArgThrPheAla 235
      814  GCGCGCCCGATGTTCCATGTTCTTCACAGAGAGACCGGTTTCCG 864

RESULT 13
US-10-225-567A-381
; Sequence 381, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-11-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent version 3.1
; SEQ ID NO 381
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-381

Alignment Scores:
Pred. No.: 2,836-23 Length: 1983
Score: 477.00 Matches: 107
Percent Similarity: 53.70% Conservative: 31
Best Local Similarity: 41.63% Mismatches: 81
Query Match: 36.41% Indels: 38
DB: 9 Gaps: 10

US-09-847-102A-68 (1-235) x US-10-225-567A-381 (1-1983)
Qy      3  ArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeuValGly 22
      136  CCGCCCGGCGAGCGCTGCGCGCTGCTGCGCGCTGCTGCTGCTGCGCGCGCGCG 195

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Qy      23  ArgAlaAlaAlaSerValaProVal-----CysGlnGlu 35
      196  CCGGCCAGTTCACAGGGGAGAGAGGATCTTCATCCCGAGACAGGCTTGTGCAGGCC 255
Qy      36  IleThrValProMetCysArgGlyIleGlyTyraAsnLeuThrIleMetProAsnIle 55
      256  ATCTTCATCCCGCTGTGACGAGATCCCTTACAAACGAGACATCATCCCAACTTGTG 315
Qy      56  AsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlu 75
      316  GCCCAGCAAGAACAGAGAGAGAGCCCTTAAGGTGACACAGTTTATCCGTGTGAAG 375
Qy      76  IlegiCysSerProAspLeuArgPhePheLeuCySthMetTyThrProIleCySleu 95
      376  GTGAGTGTGTGCGCCGGAAGTGTGCTTTCTCTGTCTCATATGAGCAACCCGTGTGACCC 435
Qy      96  ProAspTyThrAlaLeuProLeuProCySthArgSerValCySgluArgAlaLeuAlaGly 115
      436  GTG---CTGGAACAGAGCCATCCCGCGGTGCTCTATCTGTGAGCGCGCGCCAGAGGC 492
Qy      116  CysSerProLeuMetArgGlnTyArgPheAlaTPrProGluArgMetSerCysAspArg 135
      493  TCGAAGCCCTCATGAACAAGTTCGATTTCAGTGGCCGAGCCGCTGCGTGCAGAC 552
Qy      136  LeuProValLeuGlyArgAspAlaGluValLeuCyMetAspTyArgAsnArgSerGlu--- 154
      553  TTCCCGGCGGACAGGC-----GCCAGCAGATCTGCTGCGGCGAGAACACATCCAGAGAC 606
Qy      155  -----AlaThrThrAlaProProArgProPheProAlaLeuProThrIleu 169
      607  GGAGCTCCCGGCTACTACACACCGCGCGCGCGGAGCTG-----CAGCGGAGTGC 660
Qy      170  ProGlyProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGly----- 186
      661  GGGGCGACCCCGGGTGGCCCGGCGCGCGCGCTCCCGCGCTACGCGCACGCTGAG 720
Qy      187  ---ProPheValCyLeuCyArgGluProPheValProIleLeuLeuGluSerHisPro 205
      721  CACCCCTTCCACTGCGCG-----CGGCTCTCAAGCTG-----CCA 756
Qy      206  LeuTyraAsnLeuValArgThrGlyGlnValProAsnCySAlaValProCySthGlnPro 225
      757  TCCATCTCAGCTACAGATTCTGGGCGAGCGTATGTGTGCGCCCTGC---GAACCT 813
Qy      226  Ser-----PheSerAlaAspGluArgThrPheAla 235
      814  GCGCGCCCGATGTTCCATGTTCTTCACAGAGAGACCGGTTTCCG 864

RESULT 14
US-10-170-235-33965
; Sequence 33965, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CLO01380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 33965
; LENGTH: 1933
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-33965

Alignment Scores:
Pred. No.: 5,586-23 Length: 1933
Score: 472.50 Matches: 108
Percent Similarity: 54.33% Conservative: 30
Best Local Similarity: 42.52% Mismatches: 77
Query Match: 36.07% Indels: 39
DB: 8 Gaps: 11

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